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Research Article

Morphological characteristics and phylogenetic analyses reveal five new species of Hymenochaetales (Agaricomycetes, Basidiomycota) from southwestern China

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Abstract

Wood-inhabiting fungi can decompose wood materials and play a crucial role in the natural world by maintaining the equilibrium of the Earth's ecosystems. In the present study, five new wood-inhabiting fungal species belonging to the order Hymenochaetales, *Hymenochaete weishanensis*, *Lyomyces albofarinaceus*, *Lyomyces albomarginatus*, *Tubulicrinis albobadius* and *Xylodon musicola*, collected from southern China, are proposed based on a combination of morphological features and molecular evidence. *Hymenochaete weishanensis* is characterized by a coriaceous, tuberculate hymenial surface, a monomitic hyphal system with simple-septate generative hyphae, and ellipsoid to narrow ellipsoid basidiospores (4.0–5.0 × 2.0–3.0 µm); *Lyomyces albofarinaceus* is characterized by pruinose hymenial surface, a monomitic hyphal system with clamped generative hyphae, and broadly ellipsoid basidiospores (6.0–7.0 × 5.0–6.0 µm); *Lyomyces albomarginatus* is characterized by the cracked hymenial surface, clamped generative hyphae, and elliposoid basidiospores (4.0–5.5 × 2.7–3.5 µm); *Tubulicrinis albobadius* is characterized by an arachnoid hymenial surface, a monomitic hyphal system with clamped generative hyphae and cylindrical to allantoid basidiospores (4.0–6.0 × 1.5–2.2 µm) and *Xylodon musicola* is characterized by an arachnoid hymenial surface, a monomitic hyphal system with clamped generative hyphae and broadly ellipsoid to globe basidiospores (4.0–5.5 × 3.5–5.0 µm). Sequences of the internal transcribed spacers (ITS) and the large subunit (nrLSU) of the nuclear ribosomal DNA (rDNA) markers of the studied samples were generated. Phylogenetic analyses were performed using maximum likelihood, maximum parsimony, and Bayesian inference methods. Full descriptions, illustrations, and phylogenetic analysis results for the five new species are provided.

Key words: Biodiversity, Classification, Molecular systematics, New taxa, Wood-inhabiting fungi, Yunnan Province

Introduction

Fungi are well-known as a diverse group of microorganisms that play important roles in forest ecosystems (Phookamsak et al. 2019). Mushroom-forming fungi (Agaricomycetes) have the greatest morphological diversity and complexity of fungi (Varga et al. 2019). Wood-inhabiting fungi are essential to natural ecosystems for nutrient cycling and maintaining plant diversity (Drinkwater et al. 2017; Horwath 2017; Hyde et al. 2018; Wu et al. 2022; Guan et al. 2023; Yuan et al. 2023; Deng et al. 2024a, b; Dong et al. 2024; Yuan and Zhao 2024; Zhang et al. 2024). The order Hymenochaetales was described as a monotypic order to accommodate Hymenochaetaceae (Frey et al. 1977; Wu et al. 2022). Hymenochaetales is globally distributed in forest ecosystems, and it comprises 15 families and 84 genera, of which 19 genera have no certain position at the family level (Wu et al. 2022; Wang et al. 2023; Wang and Zhou 2024). Most of the species in Hymenochaetales are polypores and corticioid fungi, which show high morphological diversity and various trophic modes, including saprotrophs, parasites, and symbionts (Wang and Zhou 2024).

The genus *Hymenochaete* Lév. was erected in 1846 and typified by *H. rubiginosa* (Dicks.) Lév. *Hymenochaete* is characterized by annual to perennial, resupinate, effused-reflexed to pileate basidioma with smooth, tuberculate, lamellate, poroid or hydnoid hymenophores; a monomitic or dimitic hyphal system; presence of setae, and hyaline, thin-walled, narrowly cylindrical to globose basidiospores (Léger 1998; Parmasto 2001; He and Dai 2012; Li et al. 2024a). Léger (1998) wrote a worldwide monograph on *Hymenochaete*, providing a key to this genus. According to Index Fungorum (www.indexfungorum.org; accessed on 4 February 2025), the genus *Hymenochaete* has 362 registered names with 235 accepted species worldwide (Léger 1998; Parmasto 2001; Parmasto and Gilbertson 2005; He and Dai 2012; Parmasto 2012; He et al. 2017; Nie et al. 2017; Pacheco et al. 2018; Miettinen et al. 2019; Du et al. 2021a, b; Li et al. 2024a).

The genus *Lyomyces* P. Karst. was introduced by Karsten (1881) and is typified by *L. sambuci* (Pers.) P. Karst. *Lyomyces* comprises corticioid fungi characterized by thin, effused, membranaceous basidiomata that appear fragile in a dry state and show hymenial surface predominantly white or whitish. The hyphal system is monomitic, subicular hyphae thin- or somewhat thick-walled, while the cystidia are thin-walled with tapering, cylindrical, sub-capitate, or capitate apical parts. Basidia are utriform, and the basidiospores are colorless with thin to thick, smooth, or occasionally minutely warted walls (Yurchenko et al. 2024a). The members of *Lyomyces* grow on dead, still-attached, or fallen branches of angiosperms, on dead, wooden, or herbaceous stems, and occasionally on gymnosperm wood (Yurchenko et al. 2017; Chen and Zhao 2020). Molecular studies on *Lyomyces* and related genera have been carried out recently (Riebesehl and Langer 2017; Yurchenko et al. 2017; Viner et al. 2018; Riebesehl et al. 2019; Chen and Zhao 2020; Yuan et al. 2024). Riebesehl and Langer (2017) indicate that *Hyphodontia* s.l. should be divided into several genera as *Hastodontia* (Parmasto) Hjortstam & Ryvarden, *Hyphodontia* J. Erikss, *Kneiffiella* (Pers.) Gray, *Lagarobasidium* Jülich, *Lyomyces* and *Xylodon* (Pers.) Gray and thus thirty-five new combinations were proposed, including fourteen *Lyomyces* species (Dong et al. 2024). The *Lyomyces sambuci* complex was clarified based on ITS and 28S sequences analyses and four new species of *Lyomyces* were

described (Yurchenko et al. 2017; Dong et al. 2024). Viner et al. (2018) studied the taxonomy of *Lagarobasidium* and *Xylodon* and indicated that twelve species clustered into the *Lyomyces* clade and then grouped with the *Xylodon* clade. Phylogenetic and morphological studies on *Lyomyces* showed that *Lyomyces* grouped with *Hastodontia*, *Hyphodontia*, *Kneiffiella*, and *Xylodon*, in which the *Lyomyces* type species *L. sambuci* was sister to *L. crustosus* (Pers.) P. Karst. formed a single lineage with high support (Riebesehl et al. 2019).

The genus *Tubulicrinis* Donk, typified by *T. glebulosus* (Fr.) Donk (Donk 1956), was a member of the corticioid fungi. They are characterized by resupinate basidiomata, firmly adnate, smooth, pruinose toporulose hymenophore, a monomitic hyphal system with clamped connections on generative hyphae and conspicuous, projecting, amyloid cystidia and small basidia, and cylindrical to allantoid or globose to ellipsoid, thin-walled, smooth, IKI– (both inamyloid and indextrinoid), acyanophilous basidiospores (Donk 1956; Bernicchia and Gorjón 2010; Dong et al. 2024). So far about 46 species have been accepted in the genus worldwide (Donk 1956; Eriksson 1958; Cunningham 1963; Oberwinkler 1966; Hayashi 1974; Ryvarden 1975; Hjortstam 1981; Hjortstam et al. 1988; Rajchenberg 2002; Sharma et al. 2015; Crous et al. 2016; Gruhn et al. 2016; He et al. 2021; Dong et al. 2024). Molecular studies in the genus *Tubulicrinis* have been carried out by Larsson et al. (2006); Dai (2011); Crous et al. (2016); and Dong et al. (2024) and indicated that two *Tubulicrinis* species, *T. gracillimu* (Ellis & Everh. ex D.P. Rogers & H.S. Jacks.) G. Cunn. and *T. subulatus* (Bourdot & Galzin) Donk, formed a monophyletic lineage and then grouped with *Coltricia* clade in Hymenochaetaceae (Larsson et al. 2006). A revised checklist of corticioid and hydnoid fungi showed that six species of *Tubulicrinis* were recorded (Dai 2011); they were nested into the Tubulicrinaceae clade, which belongs to the order Hymenochaetales (Crous et al. 2016; Dong et al. 2024). Based on morphological and molecular analysis of *Tubulicrinis*, two new species were described as *T. xantha* C.L. Zhao and *T. yunnanensis* C.L. Zhao (He et al. 2021).

The genus *Xylodon* (Pers.) Gray is typified by *X. quercinus* (Pers.) Gray (Bernicchia and Gorjón 2010; Yuan and Zhao 2024). The taxa of this genus grow on rotten gymnosperm or angiosperm trunks and stumps, bamboo, and ferns (Greslebin and Rajchenberg 2000; Kotiranta and Saarenoksa 2000; Girometta et al. 2021; Guan et al. 2023; Yuan and Zhao 2024). This genus is characterized by the resupinate or effused basidiomata with a smooth, tuberculate, grandinioid, odontioid, coralloid, irpicoid, or poroid hymenophore; a monomitic or dimitic hyphal system with clamped generative hyphae; the presence of different types of cystidia; utriform or suburniform basidia; and cylindrical to ellipsoid to globose basidiospores (Gray 1821; Bernicchia and Gorjón 2010; Zhang et al. 2024; Yuan and Zhao 2024). Based on the MycoBank database (http://www.mycobank.org, accessed on 4 February 2025 and the Index Fungorum (http://www.indexfungorum.org, accessed on 4 February 2025, 241 specific and infraspecific names are registered for *Xylodon*, of which, 134 are accepted species (Chevallier 1826; Kuntze 1898; Wu 1990, 2000, 2001, 2006; Hjortstam and Ryvarden 2007, 2009; Xiong et al. 2009, 2010; Bernicchia and Gorjón 2010; Tura et al. 2011; Dai 2012; Lee and Langer 2012; Yurchenko and Wu 2014; Zhao et al. 2014; Chen et al. 2016; Kan et al. 2017a, b; Wang and Chen 2017; Viner et al. 2018, 2021; Riebesehl et al. 2019; Shi et al. 2019; Dai et al. 2021; Luo et al. 2021a, 2022; Qu and Zhao 2022; Qu et al. 2022; Guan et al. 2023; Dong et al. 2024; Yuan et al. 2024; Yurchenko et al. 2024b; Zhang et al. 2024).

The present work describes five new species of Hymenochaetales from southwest China, based on the morphology and phylogeny. To clarify the placement and relationships of these new species, we carried out a phylogenetic and taxonomic study based on the combined ITS+nLSU and ITS only sequences analyses. Full descriptions, illustrations, and comparison of five new species with closely related taxa and phylogenetic trees showing the placement of five new species within the order Hymenochaetales are provided.

Materials and methods

Sample collection and herbarium specimen preparation

The fresh fruiting bodies were collected on the fallen angiosperm branches which came from Dali, Zhaotong, and Qujing of Yunnan Province, China, and the important collection information was noted (Rathnayaka et al. 2024). The samples were photographed in situ, and fresh macroscopic details were recorded. Photographs were recorded by a Nikon D7100 camera. All the photos were focus-stacked using Helicon Focus software, and macroscopic details were recorded. Specimens were dried in an electric food dehydrator at 40 °C (Hu et al. 2022; Dong et al. 2024). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labeled (Dong et al. 2024). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The color terminology follows Petersen (1996). The micromorphological data were obtained from the dried specimens after observation under a light microscope with a magnification of 10 × 100 (Zhao et al. 2023; Dong et al. 2024). Sections were mounted in 5% KOH and 2% phloxine B dye ($C_{20}H_2Br_4C_{l-4}Na_2O_5$), and we also used other reagents, including Cotton Blue and Melzer's reagent to observe micromorphology following (Dong et al. 2024). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospores measurements. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, IKI– = both inamyloid and non-dextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores (a) measured from given number (b) of specimens).

Molecular phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The ITS region was amplified with ITS5 and ITS4 primers (White et al. 1990). The nLSU region was amplified with

the LR0R and LR7 (Vilgalys and Hester 1990; Rehner and Samuels 1994). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). The newly generated sequences were deposited in NCBI GenBank (Table 1).

The sequences were aligned in MAFFT version 7 (Katoh et al. 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). A sequence of *Thelephora ganbajun* obtained from GenBank was used as an outgroup to root trees in the ITS+nLSU analysis (Fig. 1) in the order Hymenochaetales (Wang and Zhou 2024) (TreeBASE WEB submission ID 31958). Sequence of *Hydnoporia tabacina* (Sowerby) Spirin, Miettinen & K.H. Larss. obtained from GenBank was used as an outgroup to root trees in the ITS analysis in the genus *Hymenochaete* (Fig. 2) (TreeBASE WEB submission ID 31959). Sequences of *Xylodon quercinus* (Pers.) Gray and *Xylodon ramicida* Spirin & Miettinen obtained from GenBank were used as outgroups to root trees in the ITS analysis in the genus *Lyomyces* (Fig. 3) (TreeBASE WEB submission ID 31960). A sequence of *Gyroporus castaneus* (Bull.) Quél. obtained from GenBank was used as an outgroup to root trees in the ITS analysis in the genus *Tubulicrinis* (Fig. 4) (TreeBASE WEB submission ID 31961). A sequence of *Lyomyces sambuci* (Pers.) P. Karst. obtained from GenBank was used as an outgroup to root trees in the ITS analysis in the genus *Xylodon* (Fig. 5) (TreeBASE WEB submission ID 31962).

Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian Inference (BI) analyses were applied to the combined three datasets following a previous study (Zhao and Wu 2017), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All of the characters were equally weighted, and gaps were treated as missing data. Using the heuristic search option with TBR branch swapping and 1,000 random sequence additions, trees were inferred. Max trees were set to 5,000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignments were also analyzed using maximum likelihood (ML) in RAxML-HPC2 on XSEDE v 8.2.8 with default parameters (Miller et al 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates.

jModelTest v2 (Darriba et al. 2012) was used to determine the best-fit evolution model for each dataset for the purposes of Bayesian inference (BI), Bayesian inference was performed using MrBayes 3.2.7a with a GTR+I+G model of DNA substitution and a gamma distribution rate variation across sites (Ronquist et al. 2012). The first one-fourth of all the generations were discarded as burn-ins. The majority-rule consensus tree of all the remaining trees was calculated. Branches were considered significantly supported if they received a maximum likelihood bootstrap value (BS) of ≥ 70%, a maximum parsimony bootstrap value (BT) of ≥ 70%, or Bayesian posterior probabilities (BPP) of ≥ 0.95.

Table 1. List of species, specimens, and GenBank accession number of sequences used in this study. [New species is shown in bold; * type material; – is shown data without used].

Order/Family	Species Name	Sample No.	GenBank Accession No.			References
			ITS	nLSU		
Boletales/Gyroporaceae	*Gyroporus castaneus*	JMP 0028	EU819468	–	USA	Palmer et al. (2008)
Hymenochaetales/ Chaetoporellaceae	*Echinoporia hydnophora*	LWZ 20150802-9	ON063639	ON063838	China	Wang et al. (2023)
	Kneiffiella eucalypticola	LWZ 20180509-11	MT319410	MT319142	China	Wang et al. (2021b)
	Kneiffiella subglobosa	LWZ 20180416-6	MT319413	MT319145	China	Wang et al. (2021b)
-/Hymenochaetaceae	*Basidioradulum mayi*	LWZ 20180510-18	MN017785	MN017792	Australia	Wang et al. (2021a)
	Basidioradulum radula	LWZ 20201017-62	ON063684	ON063884	China	Wang et al. (2023)
	Coltricia abieticola	Cui 10321	KX364785	KX364804	China	Bian and Dai (2017)
	Fulvoderma australe	LWZ 20190809-39b	ON063644	ON063843	China	Wang et al. (2023)
	Fulvoderma yunnanense	CLZhao 10651	OL619278	OL619278	China	Direct Submission
	Fuscoporia gilva	MSU653	JF461327	JF461327	Thailand	Insumran et al. (2012)
	Fuscoporia sinica	LWZ 20190816-19a	ON063649	ON427358	China	Wang et al. (2023)
	Hydnoporia tabacina	LWZ 20210924-26a	ON063651	ON063851	China	Wang et al. (2023)
	Hydnoporia tabacina	He 390	JQ279610	–	China	He et al.(2017)
	Hymenochaete acerosa	He 338	JQ279543	–	China	He et al.(2017)
	Hymenochaete adusta	He 207	JQ279523	–	China	He et al.(2017)
	Hymenochaete angustispora	Dai 17045	MF370592	–	China	He et al.(2017)
	Hymenochaete angustispora	Dai 17049	MF370593	–	China	He et al.(2017)
	Hymenochaete anomala	He 592	JQ279566	–	China	He et al.(2017)
	Hymenochaete asetosa	Dai 10756	JQ279559	–	China	He et al.(2017)
	Hymenochaete attenuata	He 28	JQ279526	–	China	He et al.(2017)
	Hymenochaete bambusicola	He 4116	KY425674	–	China	He et al.(2017)
	Hymenochaete berteroi	He 1488	KU975459	–	China	He et al.(2017)
	Hymenochaete biformisetosa	He 1445	KF908247	–	China	Yang and He (2014)
	Hymenochaete boddingii	MEH 66068	MN030343	–	India	Du et al.(2021a)
	Hymenochaete boddingii	MEH 69996	MN030341	–	India	Du et al.(2021a)
	Hymenochaete boddingii	MEH 66150	MN030344	–	India	Du et al.(2021a)
	Hymenochaete borbonica	CBS 731.86	MH862026	–	Netherlands	Du et al.(2021a)
	Hymenochaete cana	He 1305	KF438169	–	China	He et al.(2017)
	Hymenochaete cinnamomea	He 755	JQ279548	–	China	He et al.(2017)
	Hymenochaete colliculosa	Dai 16427	MF370595	–	China	He et al.(2017)
	Hymenochaete colliculosa	Dai 16428	MF370596	–	China	He et al.(2017)
	Hymenochaete colliculosa	Dai 16429	MF370597	–	China	He et al.(2017)
	Hymenochaete conchata	MEH 70144	MF373838	–	India	Du et al.(2021a)
	Hymenochaete contiformis	He 1166	KU975461	–	China	He et al.(2017)
	Hymenochaete cruenta	He 766	JQ279595	–	China	He et al.(2017)
	Hymenochaete cyclolamellata	Cui 7393	JQ279513	–	China	He et al.(2017)
	Hymenochaete damicornis	URM 84261	KC348466	–	Brazil	Du et al.(2021a)
	Hymenochaete damicornis	URM 84263	KC348467	–	Brazil	Du et al.(2021a)
	Hymenochaete denticulata	He 1271	KF438171	–	China	He et al. (2017)
	Hymenochaete dracaenicola	Dai 22090	MW559797	–	China	Du et al. (2021a)
	Hymenochaete dracaenicola	Dai 22096	MW559798	–	China	Du et al. (2021a)
	Hymenochaete duportii	AFTOL ID666	DQ404386	–	USA	He et al.(2017)

Order/Family	Species Name	Sample No.	GenBank Accession No.			References
			ITS	nLSU		
-/Hymenochaetaceae	*Hymenochaete epichlora*	He 525	JQ279549	–	China	He and Dai (2012)
	Hymenochaete floridea	He 536	JQ279597	–	China	He and Dai (2012)
	Hymenochaete fuliginosa	He 1188	KU975465	–	China	Du et al.(2021a)
	Hymenochaete fulva	He 640	JQ279565	–	China	He and Dai (2012)
	Hymenochaete huangshanensis	He 432	JQ279533	–	China	He and Dai (2012)
	Hymenochaete japonica	He 245	JQ279590	–	China	He and Dai (2012)
	Hymenochaete innexa	He 555	JQ279584	–	China	He and Dai (2012)
	Hymenochaete legeri	He 960	KU975469	–	China	He et al.(2017)
	Hymenochaete longispora	He 217	JQ279537	–	China	He and Dai (2012)
	Hymenochaete luteobadia	He 8	JQ279569	–	China	He and Dai (2012)
	Hymenochaete macrochloae	ARAN-Fungi 7079	MF990738	–	Spain	Du et al.(2021a)
	Hymenochaete megaspora	He 302	JQ279553	–	China	He and Dai (2012)
	Hymenochaete minor	He 933	JQ279555	–	China	He and Dai (2012)
	Hymenochaete minuscula	He 253	JQ279546	–	China	He and Dai (2012)
	Hymenochaete muroiana	He 405	JQ279542	–	China	Du et al.(2021a)
	Hymenochaete nanospora	He 475	JQ279531	–	China	He and Dai (2012)
	Hymenochaete ochromarginata	He 47	JQ279579	–	China	He and Dai (2012)
	Hymenochaete tabacina	Dai 11635	JQ279563	–	China	He and Dai (2012)
	Hymenochaete orientalis	He 4601	KY425677	–	China	He et al.(2017)
	Hymenochaete parmastoi	He 867	JQ780063	–	China	He et al.(2017)
	Hymenochaete paucisetigera	Cui 7845	JQ279560	–	China	He and Dai (2012)
	Hymenochaete quercicola	He 373	KU975474	–	China	He et al.(2017)
	Hymenochaete rhabarbarina	He 280	JQ279574	–	China	He and Dai (2012)
	Hymenochaete rheicolor	Cui 8317	JQ279529	–	China	Du et al.(2021a)
	Hymenochaete rhododendricola	He 389	JQ279577	–	China	He and Dai (2012)
	Hymenochaete rubiginosa	He 1049	JQ716407	–	China	Yang et al.(2016)
	Hymenochaete rufomarginata	He 1489	KU975477	–	China	He et al.(2017)
	Hymenochaete sharmae	CAL 1535	KY929017	–	India	Du et al.(2021a)
	Hymenochaete sharmae	66088	MK588753	–	India	Du et al.(2021a)
	Hymenochaete sinensis	CLZhao 26040	OR659001	–	China	Li et al. (2024a)
	Hymenochaete sinensis	CLZhao 26652	PQ060540	–	China	Li et al. (2024a)
	Hymenochaete separabilis	He 460	JQ279572	–	China	He and Dai (2012)
	Hymenochaete spathulata	He 685	JQ279591	–	China	He et al.(2017)
	Hymenochaete sphaericola	He 303	JQ279599	–	China	He and Dai (2012)
	Hymenochaete sphaerospora	He 715	JQ279594	–	China	He et al.(2017)
	Hymenochaete subferruginea	Cui 8122	JQ279521	–	China	Du et al.(2021a)
	Hymenochaete subferruginea	He 1598	KU975481	–	China	Du et al.(2021a)
	Hymenochaete tasmanica	He 449	JQ279582	–	China	He et al.(2017)
	Hymenochaete tenuis	He 779	JQ279538	–	China	Du et al.(2021a)
	Hymenochaete tongbiguanensis	He 1552	KF908248	–	China	He et al.(2017)
	Hymenochaete tropica	He 574	JQ279587	–	China	He et al.(2017)
	Hymenochaete ulmicola	He 864	JQ780065	–	China	He et al.(2017)
	Hymenochaete unicolor	He 468a	JQ279551	–	China	He et al.(2017)

Order/Family	Species Name	Sample No.	GenBank Accession No.			References
			ITS	nLSU		
-/Hymenochaetaceae	*Hymenochaete verruculosa*	Dai 17052	MF370594	–	China	He et al.(2017)
	Hymenochaete villosa	He 537	JQ279528	–	China	He et al.(2017)
	Hymenochaete weishanensis	**CLZhao 22615***	**PQ523357**	**PQ523363**	**China**	**Present study**
	Hymenochaete xerantica	LWZ 20190814-13b	ON063657	ON063856	China	Wang et al. (2023)
	Hymenochaete yunnanensis	He 1447	KU975486	–	China	He et al.(2017)
	Inonotus hispidus	LWZ 20180703-1	ON063659	ON063858	China	Wang et al. (2023)
	Phellinus piceicola	LWZ 20190921-5	ON063662	ON063862	China	Wang et al. (2023)
	Phylloporia oreophila	LWZ 20190811-27a	ON063665	ON063865	China	Wang et al. (2023)
	Porodaedalea laricis	LWZ 20190724-9	ON063668	ON063868	China	Wang et al. (2023)
	Sanghuangporus weigelae	LWZ 20210623-2a	ON063671	ON063870	China	Wang et al. (2023)
	Trichaptum biforme	LWZ 20210919-32a	ON063701	ON063901	China	Wang et al. (2023)
	Trichaptum fuscoviolaceum	LWZ 20210918-5b	ON063703	ON063903	China	Wang et al. (2023)
	Hyphodontia arguta	3216b	DQ873605	DQ873605	Sweden	Larsson et al. (2006)
	Hyphodontia borbonica	FR 0219441	KR349240	KR349240	Reunion	Riebesehl and Langer (2017)
	Hyphodontia pachyspora	LWZ 20170908-5	MT319426	MT319160	China	Wang et al. (2021b)
	Hyphodontia pallidula	Kotiranta_18839	OP620785	OP620785	Finland	Viner et al. (2023)
	Hyphodontia zhixiangii	LWZ 20170818-13	MT319420	MT319151	China	Wang er al. (2021b)
-/Odonticiaceae	*Leifia brevispora*	LWZ 20170820-48	MK343470	MK343474	China	Liu et al. (2019)
	Leifia flabelliradiata	KG Nilsson 36270	DQ873635	DQ873635	Sweden	Larsson et al. (2006)
	Odonticium romellii	KHL s. n.	DQ873639	DQ873639	Norway	Larsson et al. (2006)
-/Peniophorellaceae	*Peniophorella praetermissa*	LWZ 20180903-14	ON063686	ON063886	China	Wang et al. (2023)
	Peniophorella pubera	LWZ 20210624-16b	ON063687	ON063887	China	Wang et al. (2023)
	Peniophorella rude	LWZ 20171026-7	ON063688	ON063888	China	Wang et al. (2023)
	Peniophorella subpraetermissa	LWZ 20190816-3b	ON063689	ON063889	China	Wang et al. (2023)
-/Repetobasidiaceae	*Repetobasidium conicum*	KHL 12338	DQ873647	DQ873647	USA	Larsson et al. (2006)
	Repetobasidium mirificum	FP-133558-sp	–	AY293208	USA	Binder et al. (2005)
-/Resiniciaceae	*Resinicium austroasianum*	LWZ 20191208-11	ON063691	ON063891	China	Wang et al. (2023)
	Resinicium bicolor	AFTOL-810	DQ218310	AY586709	USA	Larsson et al. (2004)
	Resinicium friabile	LWZ 20210923-23a	ON063692	ON427362	China	Wang et al. (2023)
-/Rickenellaceae	*Rickenella danxiashanensis*	GDGM45513	MF326424	–	China	Zhang et al. (2018)
	Rickenella fibula	PBM 2503	DQ241782	MF318953	USA	Lutzoni et al. (2004)
-/Rigidoporaceae	*Leucophellinus hobsonii*	Cui 6468	KT203288	KT203309	China	Direct Submission
	Leucophellinus irpicoides	Yuan 2690	KT203289	KT203310	China	Direct Submission
	Rigidoporus cirratus	LWZ 20170818-16	ON427472	ON427355	China	Wang et al. (2023)
	Rigidoporus populinus	LWZ 20190811-39a	ON063674	ON063874	China	Wang et al. (2023)
-/Schizocorticiaceae	*Schizocorticium lenis*	LWZ 20180922-61	ON063698	ON063898	China	Wang et al. (2023)
	Schizocorticium magnosporum	Wu 1510-34	MK405351	MK405337	China	Wu et al. (2021)
	Schizocorticium mediosporum	LWZ 20180921-7	ON063696	ON063896	China	Wang et al. (2023)
	Schizocorticium mediosporum	Chen 2456	MK405359	MK405345	China	Wu et al. (2021)
	Schizocorticium parvisporum	GC 1508-127	MK405361	MK405347	China	Wu et al. (2021)
-/Schizoporaceae	*Fasciodontia brasiliensis*	MSK-F 7245a	MK575201	MK598734	Brazil	Yurchenko et al. (2020)

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			ITS	nLSU		
-/Schizoporaceae	*Fasciodontia yunnanensis*	LWZ 20190811-50a	ON063675	ON427360	China	Wang et al. (2023)
	Lyomyces albofarinaceus	**CLZhao 33479***	**PQ523359**	–	**China**	**Present study**
	Lyomyces albofarinaceus	**CLZhao 26661**	**PQ523360**	–	**China**	**Present study**
	Lyomyces albopulverulentus	CLZhao 21478	OP730712	–	China	Guan et al (2023)
	Lyomyces allantosporus	KAS-GEL4933	KY800401	–	France	Yurchenko et al. (2017)
	Lyomyces allantosporus	FR-0249548	KY800397	–	France	Yurchenko et al. (2017)
	Lyomyces austro-occidentalis	LWZ 20190816-40a	MZ262538	–	China	Liu et al. (2024)
	Lyomyces bambusinus	CLZhao 4831	MN945968	–	China	Chen and Zhao (2020)
	Lyomyces bambusinus	CLZhao 4808	MN945970	–	China	Chen and Zhao (2020)
	Lyomyces boquetensis	EYu 190727-12	PP471797	–	Panama	Yurchenko et al. (2024a)
	Lyomyces cremeus	CLZhao 4138	MN945974	–	China	Chen and Zhao (2020)
	Lyomyces cremeus	CLZhao 8295	MN945972	–	China	Chen and Zhao (2020)
	Lyomyces crustosus	TASM:YG G39	MF382993	–	Uzbekistan	Gafforov et al. (2017)
	Lyomyces crustosus	LWZ 20170815-23	MT319465	MT319201	China	Wang et al. (2021b)
	Lyomyces crystallina	LWZ 20190810-6b	OQ540901	–	China	Liu et al. (2024)
	Lyomyces daweishanensis	CLZhao 18344	OR094474	–	China	Dong et al. (2024)
	Lyomyces densiusculus	Ryvarden 44818	OK273853	–	Uganda	Viner et al. (2021)
	Lyomyces denudatus	Ryvarden 19256	ON980759	–	Argentina	Viner and Miettinen (2022)
	Lyomyces denudatus	Ryvarden 19436	ON980760	–	Argentina	Viner and Miettinen (2022)
	Lyomyces elaeidicola	LWZ20180411-20	MT319458	–	China	Wang et al. (2021b)
	Lyomyces elaeidicola	LWZ20180411-19	MT319457	–	China	Wang et al. (2021b)
	Lyomyces erastii	TASM:YG 022	MF382992	–	Uzbekistan	Gafforov et al. (2017)
	Lyomyces erastii	23cSAMHYP	JX857800	–	Spain	Unpublished
	Lyomyces fimbriatus	Wu910620-7	MK575209	–	China	Yurchenko et al. (2020)
	Lyomyces fimbriatus	Wu911204-4	MK575210	–	China	Yurchenko et al. (2020)
	Lyomyces albomarginatus	**CLZhao 22551***	**PQ644120**	**PQ644121**	**China**	**Present study**
	Lyomyces fissuratus	CLZhao 4352	MW713742	–	China	Luo et al. (2021b)
	Lyomyces fissuratus	CLZhao 4291	MW713738	–	China	Luo et al. (2021b)
	Lyomyces fumosus	CLZhao 8188	MW713744	–	China	Luo et al. (2021b)
	Lyomyces gatesiae	LWZ20180515-3	MT319447	–	China	Wang et al. (2021b)
	Lyomyces gatesiae	LWZ20180515-32	MT319448	–	China	Wang et al. (2021b)
	Lyomyces granulosus	KAS-GEL1662	PP471799	–	Costa Rica	Yurchenko et al. (2024a)
	Lyomyces griseliniae	KHL 12971 (GB)	DQ873651	–	Costa Rica	Larsson et al. (2006)
	Lyomyces griseliniae	CBS:126042	MH864057	–	New Zealand	Vu et al. (2018)
	Lyomyces guttulatus	LWZ 20200921-29a	OQ540899	–	China	Liu et al. (2024)
	Lyomyces guttulatus	LWZ 20190810-20b	OQ540898	–	China	Liu et al. (2024)

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-/Schizoporaceae	*Lyomyces hengduanensis*	CLZhao 20627	OR793233	–	China	Yuan and Zhao (2024)
	Lyomyces hengduanensis	CLZhao 25551	OR658999	–	China	Yuan and Zhao (2024)
	Lyomyces incanus	CLZhao 22813	OR094480	–	China	Dong et al. (2024)
	Lyomyces incanus	CLZhao 22900	OR094481	–	China	Dong et al. (2024)
	Lyomyces juniperi	FR-0261086	KY081799	–	France	Riebesehl and Langer (2017)
	Lyomyces leptocystidiatus	LWZ 20170814-14	MT319429	MT319163	China	Wang et al. (2021b)
	Lyomyces leptocystidiatus	LWZ 20170818-1	MT326514	–	China	Wang et al. (2021b)
	Lyomyces leptocystidiatus	LWZ 20170818-2	MT326513	–	China	Wang et al. (2021b)
	Lyomyces lincangensis	CLZhao 22966	OR094487	–	China	Dong et al. (2024)
	Lyomyces luteoalbus	CLZhao 18211	OR094485	–	China	Dong et al. (2024)
	Lyomyces luteoalbus	CLZhao 18347	OR094486	–	China	Dong et al. (2024)
	Lyomyces macrosporus	CLZhao 4516	MN945977	–	China	Chen and Zhao (2020)
	Lyomyces mascarensis	KAS-GEL4833	KY800399	–	France	Yurchenko et al. (2020)
	Lyomyces mascarensis	KAS-GEL4908	KY800400	–	France	Yurchenko et al. (2020)
	Lyomyces microfasciculatus	CLZhao 5109	MN954311	–	China	Chen and Zhao (2020)
	Lyomyces napoensis	EYu 190720-18	PP471800	–	Ecuador	Yurchenko et al. (2024a)
	Lyomyces neocrustosus	EYu 190728-14	PP471801	–	Panama	Yurchenko et al. (2024a)
	Lyomyces niveomarginatus	CLZhao 16360	PP537949	–	China	Yuan and Zhao (2024)
	Lyomyces niveus	CLZhao 6431	MZ262541	–	China	Luo et al. (2021b)
	Lyomyces niveus	CLZhao 6442	MZ262542	–	China	Luo et al. (2021b)
	Lyomyces ochraceoalbus	CLZhao 4385	MZ262535	–	China	Luo et al. (2021b)
	Lyomyces ochraceoalbus	CLZhao 4725	MZ262536	–	China	Luo et al. (2021b)
	Lyomyces oleifer	KAS-Ec47	PP471802	–	Ecuador	Yurchenko et al. (2024a)
	Lyomyces orarius	EYu 190724-1	PP471805	–	Ecuador	Yurchenko et al. (2024a)
	Lyomyces organensis	MSK7247	KY800403	–	Brazil	Yurchenko et al. (2017)
	Lyomyces orientalis	GEL3376	DQ340325	–	Germany	Yurchenko et al. (2017)
	Lyomyces pantropicus	EYu 190727-23b	PP471808	–	Panama	Yurchenko et al. (2024a)
	Lyomyces parvus	KAS-GEL1599	PP471810	–	Costa Rica	Yurchenko et al. (2024a)
	Lyomyces pruni	GEL2327	DQ340312	–	Germany	Larsson et al. (2006)
	Lyomyces pruni	Ryberg 021018 (GB)	DQ873624	–	Sweden	Larsson et al. (2006)
	Lyomyces punctatomarginatus	CLZhao 22699	OR844492	–	China	Li et al. (2024b)
	Lyomyces punctatomarginatus	CLZhao 11629	OR844491	–	China	Li et al. (2024b)
	Lyomyces qujingensis	CLZhao 27462	OR167768	–	China	Dong et al. (2024)
	Lyomyces sambuci	KAS-JR7	KY800402	–	Germany	Yurchenko et al. (2017)

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			ITS	nLSU		
-/Schizoporaceae	*Lyomyces sambuci*	83SAMHYP	JX857721	–	Sweden	Yurchenko et al. (2017)
	Lyomyces sambuci	LWZ 20180905-1	MT319444	MT319178	China	Wang et al. (2021b)
	Lyomyces sceptrifer	KAS-Ec661	PP471811	–	Ecuador	Yurchenko et al. (2024a)
	Lyomyces sinensis	CLZhao 27391	OR167769	–	China	Dong et al. (2024)
	Lyomyces sinensis	CLZhao 27464	OR167770	–	China	Dong et al. (2024)
	Lyomyces subcylindricus	EYu 190727-25	PP471817	–	Panama	Yurchenko et al. (2024a)
	Lyomyces tasmanicus	LWZ 20180515–17	OQ540900	–	China	Liu et al. (2024)
	Lyomyces vietnamensis	TNM F9073	JX175044	–	China	Yurchenko et al. (2017)
	Lyomyces wuliangshanensis	CLZhao 4108	MN945980	–	China	Chen and Zhao (2020)
	Lyomyces wuliangshanensis	CLZhao 4167	MN945979	–	China	Chen and Zhao (2020)
	Lyomyces wumengshanensis	CLZhao 29374	OR803021	–	China	Yuan and Zhao (2024)
	Lyomyces wumengshanensis	CLZhao 31486	OR899208	–	China	Yuan and Zhao (2024)
	Lyomyces yunnanensis	CLZhao 9375	OP730710	–	China	Guan et al. (2023)
	Lyomyces yunnanensis	CLZhao 10041	OP730709	–	China	Guan et al. (2023)
	Lyomyces zhaotongensis	CLZhao 32878	PP537950	–	China	Yuan et al. (2024)
	Xylodon acuminatus	Larsson 16029	ON197552	–	Brazil	Viner et al. (2023)
	Xylodon acystidiatus	LWZ 20180514-9	MT319474	–	China	Wang et al. (2021b)
	Xylodon afromontanus	O-F-904012	OQ645463	–	Rwanda	Yurchenko et al. (2024a)
	Xylodon angustisporus	Ryvarden 50691b	OK273831	–	Cameroon	Viner et al. (2021)
	Xylodon apacheriensis	Canfield 180	KY081800	–	USA	Wang et al. (2021b)
	Xylodon asiaticus	CLZhao 10368	OM959479	–	China	Unpublished
	Xylodon asper	Spirin 11923	OK273838	–	Russia	Viner et al. (2021)
	Xylodon astrocystidiatus	TNM F24764	NR154054	–	USA	Yurchenko and Wu (2014)
	Xylodon attenuatus	Spirin 8775	MH324476	–	Russia	Wang et al. (2021b)
	Xylodon australis	LWZ 20180509-8	MT319503	–	China	Wang et al. (2021b)
	Xylodon bambusinus	CLZhao 9174	MW394657	–	China	Ma and Zhao (2021)
	Xylodon bamburesupinus	CLZhao 23088	OR167773	–	China	Dong et al. (2024)
	Xylodon borealis	JS 26064	AY463429	–	Sweden	Larsson et al. (2004)
	Xylodon brevisetus	JS 17863	AY463428	–	Sweden	Larsson et al. (2004)
	Xylodon cremeoparinaceus	CLZhao 23388	PP537951	–	China	Yuan and Zhao (2024)
	Xylodon crystalliger	KUN 2312	NR166242	–	USA	Viner et al. (2018)
	Xylodon cymosus	Miettinen 19606	ON197554	–	Finland	Viner et al. (2023)
	Xylodon cystidiatus	FR-0249200	MH880195	–	Germany	Wang et al. (2021b)
	Xylodon damansaraensis	LWZ 20180417-23	MT319499	–	China	Wang et al. (2021b)
	Xylodon daweishanensis	CLZhao 18357	OP730715	–	China	Guan et al. (2023)
	Xylodon detriticus	Zíbarová 30.10.17	MH320793	–	Russia	Wang et al. (2021b)
	Xylodon dissiliens	Ryvarden 44817	OK273856	–	Finland	Viner et al. (2021)

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			ITS	nLSU		
-/Schizoporaceae	*Xylodon echinatus*	OM 18237	OQ645464	–	Germany	Yurchenko et al. (2024a)
	Xylodon filicinus	MSK-F 12869	MH880199	–	Germany	Wang et al. (2021b)
	Xylodon fissilis	CLZhao 18740	OR096211	–	China	Dong et al. (2024)
	Xylodon fissuratus	CLZhao 9407	OP730714	–	China	Guan et al. (2023)
	Xylodon flaviporus	FR-0249797	MH880201	–	Germany	Wang et al. (2021b)
	Xylodon flocculosus	CLZhao 18342	MW980776	–	China	Unpublished
	Xylodon follis	FR-0249814	MH880204	–	Germany	Wang et al. (2021b)
	Xylodon gloeocystidiifer	BLS M-5232	OQ645467	–	Germany	Yurchenko et al. (2024a)
	Xylodon gossypinus	CLZhao 8375	MZ663804	–	China	Luo et al. (2021a)
	Xylodon grandineus	CLZhao 6425	OM338090	–	China	Luo et al. (2022)
	Xylodon hastifer	K(M) 172400	NR166558	–	USA	Riebesehl and Langer (2017)
	Xylodon heterocystidiatus	Wei 17-314	MT731753	–	China	Wu et al. (2021)
	Xylodon hjortstamii	Gorjon 3187	ON188816	–	Finland	Direct Submission
	Xylodon hydnoides	CLZhao 17991	OR096203	–	China	Dong et al. (2024)
	Xylodon hyphodontinus	KAS-GEL9222	MH880205	–	Germany	Riebesehl et al. (2019)
	Xylodon jacobaeus	MA-Fungi 91340	MH430073	–	Spain	Wang et al. (2021b)
	Xylodon kunmingensis	TUB-FO 42565	MH880198	–	Germany	Wang et al. (2021b)
	Xylodon laceratus	CLZhao 9892	OL619258	–	China	Qu et al. (2022)
	Xylodon lagenicystidiatus	LWZ 20180515-14	MT319633	–	China	Wang et al. (2021b)
	Xylodon lagenicystidiatus	LWZ 20180513-16	MT319634	–	China	Wang et al. (2021b)
	Xylodon lanatus	CFMR FP-101864-A	OQ645474	–	Germany	Yurchenko et al. (2024a)
	Xylodon laxiusculus	Ryvarden 44877	OK273827	–	Finland	Viner et al. (2021)
	Xylodon lenis	Wu 890714-3	KY081802	–	Germany	Yurchenko et al. (2024a)
	Xylodon luteodontioides	CLZhao 3207	MH114740	–	China	Yuan and Zhao (2024)
	Xylodon luteodontioides	CLZhao 18494	PP505422	–	China	Yuan and Zhao (2024)
	Xylodon macrosporus	CLZhao 10226	MZ663809	–	China	Luo et al. (2021a)
	Xylodon magallanesii	MA: Fungi:90397	MT158729	–	Spain	Fernandez-Lopez et al. (2020)
	Xylodon mantiqueirensis	MV 529	OQ645478	–	Germany	Yurchenko et al. (2024a)
	Xylodon mollissimus	LWZ 20160318-3	KY007517	–	China	Kan et al. (2017b)
	Xylodon montanus	CLZhao 8179	OL619260	–	China	Qu et al. (2022)
	Xylodon muchuanensis	LWZ 20200819-3a	OQ540903	–	China	Liu et al. (2024)
	Xylodon musicola	**CLZhao 35567***	**PQ523358**	–	**China**	**Present study**
	Xylodon neotropicus	MV 580	OQ645479	–	Germany	Yurchenko et al. (2024a)
	Xylodon nesporii	LWZ 20180921-35	MT319655	–	China	Wang et al. (2021b)
	Xylodon nesporii	LWZ 20190814-17a	ON063679	ON063879	China	Wang et al. (2023)
	Xylodon niemelaei	CLZhao 3746	MK269038	–	China	Unpublished
	Xylodon nongravis	GC 1412-22	KX857801	–	China	Chen et al. (2017)
	Xylodon nothofagi	ICMP 13842	AF145583	–	Sweden	Wang et al. (2021b)
	Xylodon olivaceobubalinus	CLZhao 25174	OR167772	–	China	Dong et al. (2024)

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			ITS	nLSU		
-/Schizoporaceae	*Xylodon ovisporus*	LWZ 20170815-31	MT319666	–	China	Wang et al. (2021b)
	Xylodon ovisporus	LWZ 20190817-6b	ON063680	ON063880	China	Wang et al. (2023)
	Xylodon papillosus	CBS 114.71	MH860026	–	Germany	Vu et al. (2018)
	Xylodon paradoxus	Dai 14983	MT319519	–	China	Wang et al. (2021b)
	Xylodon patagonicus	ICMP 13832	AF145581	–	Sweden	Wang et al. (2021b)
	Xylodon pingbianensis	CLZhao 19029	OR096208	–	China	Dong et al. (2024)
	Xylodon poroides	CLZhao 17845	PP505420	–	China	Yuan and Zhao (2024)
	Xylodon pruinosus	Spirin 2877	MH332700	–	Russia	Wang et al. (2021b)
	Xylodon pruniaceus	Ryvarden 11251	OK273828	–	Finland	Viner et al. (2021)
	Xylodon pseudolanatus	FP-150922	MH880220	–	Germany	Wang et al. (2021b)
	Xylodon pseudotropicus	Dai 10768	KF917543	–	China	Wang et al. (2021b)
	Xylodon puerensis	CLZhao 8142	OP730720	–	China	Guan et al. (2023)
	Xylodon punctus	CLZhao 17691	OM338092	–	China	Luo et al. (2022)
	Xylodon punctus	CLZhao 17908	OM338093	–	China	Luo et al. (2022)
	Xylodon punctus	CLZhao 17916	OM338094	–	China	Luo et al. (2022)
	Xylodon quercinus	Spirin 12030	OK273841	–	Finland	Viner et al. (2021)
	Xylodon raduloides	FCUG 2433	AF145570	–	Sweden	Wang et al. (2021b)
	Xylodon ramicida	Spirin 7664	NR138013	–	Russia	Direct Submission
	Xylodon reticulatus	Wu 1109-178	KX857805	–	China	Wang et al. (2021b)
	Xylodon reticulatus	GC 1512-1	KX857808	–	China	Wang et al. (2021b)
	Xylodon rimosissimus	LWZ 20180904-28	ON063682	ON063882	China	Wang et al. (2023)
	Xylodon rhizomorphus	Dai 12367	NR154067	–	China	Zhao et al. (2014)
	Xylodon rhododendricola	LWZ 20180513-9	MT319621	–	China	Wang et al. (2021b)
	Xylodon serpentiformis	LWZ 20190816-12a	ON063683	ON063883	China	Wang et al. (2023)
	Xylodon sinensis	CLZhao 9197	MZ663810	–	China	Luo et al. (2021a)
	Xylodon sinensis	CLZhao 11120	MZ663811	–	China	Luo et al. (2021a)
	Xylodon spathulatus	LWZ 20180804-10	MT319646	–	China	Wang et al. (2021b)
	Xylodon subclavatus	FO 42167	MH880232	–	China	Wang et al. (2021b)
	Xylodon subflaviporus	TNM F29958	NR184880	–	USA	Chen et al. (2017)
	Xylodon submucronatus	Renvall 1602	OK273830	–	Finland	Viner et al. (2021)
	Xylodon subserpentiformis	LWZ 20180512-16	MT319486	–	China	Wang et al. (2021b)
	Xylodon subtilissimus	Spirin 12228	ON188818	–	Finland	Direct Submission
	Xylodon subtropicus	LWZ 20180510-24	MT319541	–	China	Wang et al. (2021b)
	Xylodon taiwanianus	CBS 125875	MH864080	–	New Zealand	Vu et al. (2018)
	Xylodon tropicus	CLZhao 3351	OL619261	–	China	Qu et al. (2022)
	Xylodon ussuriensis	KUN 1989	NR166241	–	Russia	Direct Submission
	Xylodon verecundus	KHL 12261	DQ873642	–	USA	Wang et al. (2021b)
	Xylodon victoriensis	LWZ 20180510-29	MT319487	–	China	Wang et al. (2021b)
	Xylodon wenshanensis	CLZhao 15729	OM338097	–	China	Luo et al. (2022)
	Xylodon wumengshanensis	CLZhao 32517	PP645439	–	China	Yuan and Zhao (2024)
	Xylodon xinpingensis	CLZhao 9174	MW394657	–	China	Ma and Zhao (2021)
	Xylodon yarraensis	LWZ 20180510-5	MT319639	–	China	Wang et al. (2021b)
	Xylodon yunnanensis	LWZ 20180922-47	MT319660	–	China	Wang et al. (2021b)

Order/Family	Species Name	Sample No.	GenBank Accession No.			References
			ITS	nLSU		
-/Sideraceae	*Sidera lenis*	Miettinen 11036	FN907914	FN907914	Finland	Miettinen and Larsson (2011)
	Sidera minutipora	Cui 16720	MN621349	MN621348	Australia	Du et al. (2020b)
	Sidera srilankensis	Dai 19654	MN621344	MN621346	Sri Lanka	Du et al. (2020b)
	Sidera tenuis	Dai 18697	MK331865	MK331867	Singapore	Liu et al. (2022)
	Sidera tibetica	Dai 21057	MW198484	MW192009	Belarus	Liu et al. (2022)
-/Skvortzoviaceae	*Skvortzovia dabieshanensis*	LWZ 20210918-15b	ON063694	ON063894	China	Wang et al. (2023)
	Skvortzovia pinicola	LWZ 20210623-18b	ON063695	ON063895	China	Wang et al. (2023)
	Skvortzovia qilianensis	LWZ 20180904-20	ON063693	ON063893	China	Wang et al. (2023)
	Skvortzovia yunnanensis	CLZhao 16084	MW472754	MW473473	China	Dong et al. (2021)
-/Tubulicrinaceae	*Tubulicrinis accedens*	ACD0414	OL756001	–	USA	Unpublished
	Tubulicrinis albobadius	**CLZhao 26202***	**PQ523361**	**PQ523364**	**China**	**Present study**
	Tubulicrinis albobadius	**CLZhao 26330**	**PQ523362**	**PQ523365**	**China**	**Present study**
	Tubulicrinis australis	MA Fungi:88838	KX017591	–	Spain	Unpublished
	Tubulicrinis australis	MA Fungi:88839	KX017593	–	Chile	Unpublished
	Tubulicrinis borealis	DK14_93	OL436811	–	USA	Unpublished
	Tubulicrinis calothrix	LWZ 20210919-1b	ON063704	–	China	Wang et al. (2023)
	Tubulicrinis chaetophorus	Spirin 12616 (H)	ON188814	–	Slovenia	Direct Submission
	Tubulicrinis chaetophorus	UC2023055	KP814255	–	USA	Rosenthal et al. (2017)
	Tubulicrinis chaetophorus	UC2023059	KP814233	–	USA	Rosenthal et al. (2017)
	Tubulicrinis glebulosus	LWZ 20180903-13	ON063705	ON063905	China	Wang et al. (2023)
	Tubulicrinis glebulosus	DK16_14	OL436905	–	USA	Unpublished
	Tubulicrinis glebulosus	UC2023229	KP814463	–	Canada	Rosenthal et al. (2017)
	Tubulicrinis globisporus	KHL 12133 (GB)	DQ873655	–	Sweden	Larsson et al. (2006)
	Tubulicrinis gracillimus	PDD 95851	HQ533047	–	New Zealand	Unpublished
	Tubulicrinis hirtellus	KHL 11717 (GB)	DQ873657	–	Sweden	Larsson et al. (2006)
	Tubulicrinis inornatus	KHL 11763 (GB)	DQ873659	–	Sweden	Larsson et al. (2006)
	Tubulicrinis inornatus	OTU782	MT596347	–	Japan	Unpublished
	Tubulicrinis martinicensis	GG-MAR12-206	NR_163282	–	France	Unpublished
	Tubulicrinis pini	CLZhao 6881	OR096210	–	China	Dong et al. (2024)
	Tubulicrinis subulatus	UC2023072	KP814430	–	USA	Rosenthal et al. (2017)
	Tubulicrinis subulatus	LWZ 20190914-7	ON063706	ON063906	China	Wang et al. (2023)
	Tubulicrinis xantha	CLZhao 2868	MT153874	–	China	He et al. (2020)
	Tubulicrinis xantha	CLZhao 2869	MT153875	–	China	He et al. (2020)
	Tubulicrinis yunnanensis	CLZhao 3418	MT153879	–	China	He et al. (2020)
	Tubulicrinis yunnanensis	CLZhao 9717	MT153880	–	China	He et al. (2020)
-/Umbellaceae	*Umbellus sinensis*	LWZ 20190615-27	OR242616	OR236212	China	Wang and Zhou (2024)
	Umbellus sinensis	LWZ 20190615-39	OR242617	OR236213	China	Wang and Zhou (2024)
-/Incertae sedis	*Alloclavaria purpurea*	M. Korhonen 10305	MF319044	MF318895	Finland	Unpublished
	Atheloderma mirabile	TAA 169235	DQ873592	DQ873592	Estonia	Larsson et al. (2006)

Order/Family	Species Name	Sample No.	GenBank Accession No.			References
			ITS	nLSU		
-/Incertae sedis	*Blasiphalia pseudogrisella*	P. Joijer 4118	MF319047	MF318898	Finland	Unpublished
	Bryopistillaria sagittiformis	IO.14.164	MT232349	MT232303	Sweden	Olariaga et al. (2020)
	Cantharellopsis prescotii	H6059300	MF319051	MF318903	Finland	Unpublished
	Contumyces vesuvianus	203608	–	MF318913	Italy	Unpublished
	Ginnsia viticola	Wu 0010-29	MN123802	GQ470670	China	Wu et al. (2021)
	Globulicium hiemale	Hjm 19007	DQ873595	DQ873595	Sweden	Larsson et al. (2006)
	Gyroflexus brevibasidiata	IO.14.230	MT232351	MT232305	Sweden	Olariaga et al. (2020)
	Hastodontia halonata	HHB-17058	MK575207	MK598738	Mexico	Yurchenko et al. (2020)
	Hastodontia hastata	KHL 14646	MH638232	MH638232	Norway	Larsson (2007)
	Lawrynomyces capitatus	KHL 8464	DQ677491	DQ677491	Sweden	Larsson (2007)
	Loreleia marchantiae	Lutzoni 930826-1	U66432	U66432	USA	Lutzoni F (1997)
	Lyoathelia laxa	Spirin 8810a	MT305998	MT305998	USA	Sulistyo et al. (2021)
	Muscinupta laevis	V. Haikonen 19745	MF319066	MF318921	Finland	Unpublished
	Sphaerobasidium minutum	KHL 11714	DQ873652	DQ873653	Finland	Larsson et al. (2006)
	Tsugacorticium kenaicum	CFMR HHB17347	–	JN368221	USA	Nakasone (2012)
Polyporales/ Fomitopsidaceae	*Fomitopsis pinicola*	AFTOL 770	AY854083	AY684164	USA	Lutzoni et al. (2004)
-/Grifolaceae	*Grifola frondosa*	AFTOL 701	AY854084	AY629318	USA	Lutzoni et al. (2004)
-/Thelephoraceae	*Thelephora ganbajun*	ZRL20151295	LT716082	KY418908	China	Zhao et al. (2017)

Results

Sequence similarity search

The ITS+nLSU dataset (Fig. 1) comprised 80 specimens representing 77 species of the phylogeny of the order Hymenochaetales. The dataset had an aligned length of 2,548 characters, of which 1,018 characters are constant, 476 are variable and parsimony uninformative, and 1,054 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 10768, CI = 0.2612, HI = 0.7388, RI = 0.4087, and RC = 0.1068). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.044070 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS) = 645.

The ITS dataset (Fig. 2) comprised 78 specimens representing 69 species of the one new species and related species in the genus *Hymenochaete*. The dataset had an aligned length of 470 characters, of which 209 characters are constant, 35 are variable and parsimony uninformative, and 226 are parsimony informative. Maximum parsimony analysis yielded 68 equally parsimonious trees (TL = 1574, CI = 0.3018, HI = 0.6982, RI = 0.6876, and RC = 0.2075). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies =

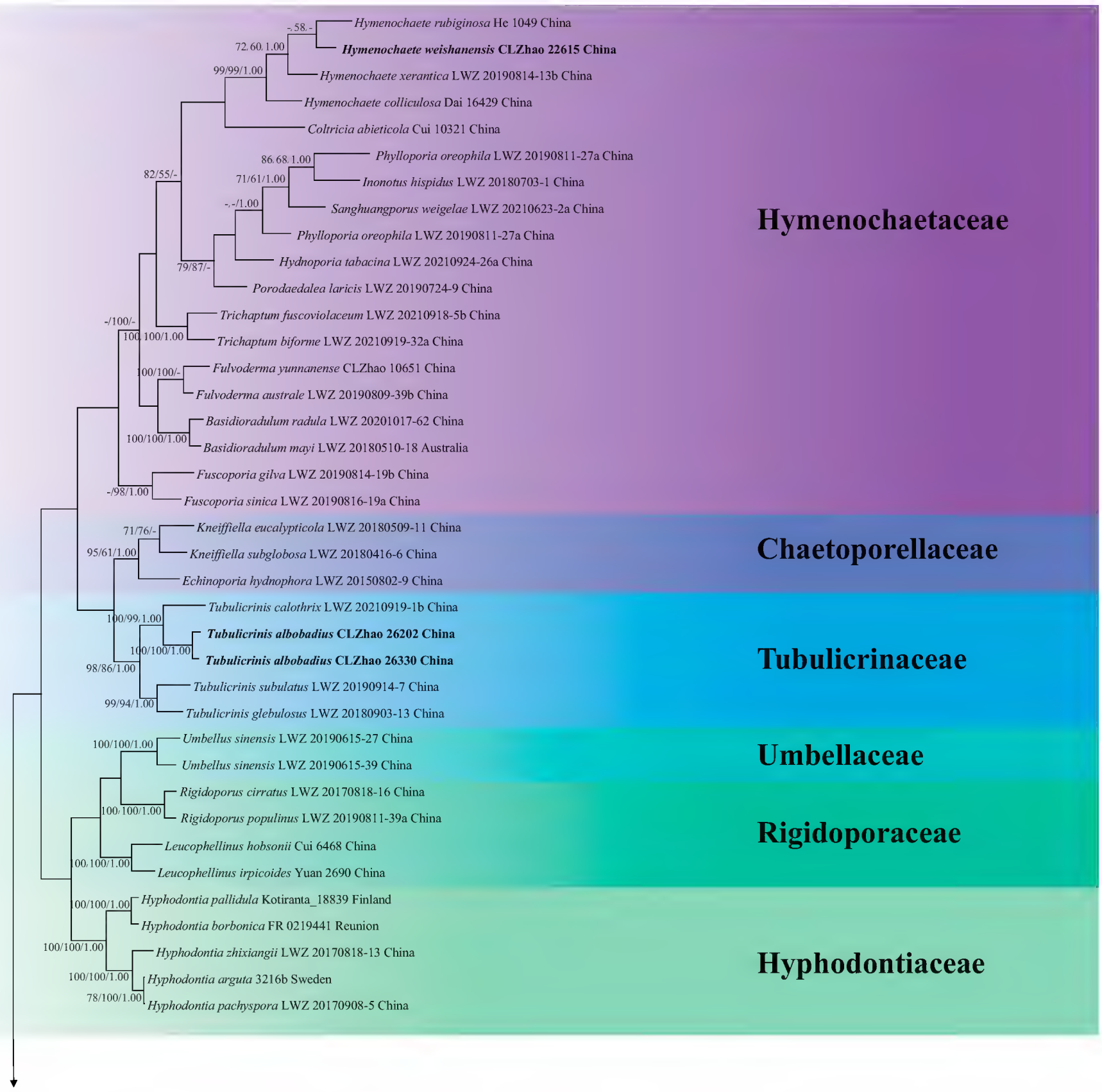
Hymenochaete rubiginosa He 1049 China
Hymenochaete weishanensis CLZhao 22615 China
Hymenochaete xerantica LWZ 20190814-13b China
Hymenochaete colliculosa Dai 16429 China
Coltricia abieticola Cui 10321 China
Phylloporia oreophila LWZ 20190811-27a China
Inonotus hispidus LWZ 20180703-1 China
Sanghuangporus weigelae LWZ 20210623-2a China
Phylloporia oreophila LWZ 20190811-27a China
Hydnoporia tabacina LWZ 20210924-26a China
Porodaedalea laricis LWZ 20190724-9 China
Trichaptum fuscoviolaceum LWZ 20210918-5b China
Trichaptum biforme LWZ 20210919-32a China
Fulvoderma yunnanense CLZhao 10651 China
Fulvoderma australe LWZ 20190809-39b China
Basidioradulum radula LWZ 20201017-62 China
Basidioradulum mayi LWZ 20180510-18 Australia
Fuscoporia gilva LWZ 20190814-19b China
Fuscoporia sinica LWZ 20190816-19a China
Kneiffiella eucalypticola LWZ 20180509-11 China
Kneiffiella subglobosa LWZ 20180416-6 China
Echinoporia hydnophora LWZ 20150802-9 China
Tubulicrinis calothrix LWZ 20210919-1b China
Tubulicrinis albobadius CLZhao 26202 China
Tubulicrinis albobadius CLZhao 26330 China
Tubulicrinis subulatus LWZ 20190914-7 China
Tubulicrinis glebulosus LWZ 20180903-13 China
Umbellus sinensis LWZ 20190615-27 China
Umbellus sinensis LWZ 20190615-39 China
Rigidoporus cirratus LWZ 20170818-16 China
Rigidoporus populinus LWZ 20190811-39a China
Leucophellinus hobsonii Cui 6468 China
Leucophellinus irpicoides Yuan 2690 China
Hyphodontia pallidula Kotiranta_18839 Finland
Hyphodontia borbonica FR 0219441 Reunion
Hyphodontia zhixiangii LWZ 20170818-13 China
Hyphodontia arguta 3216b Sweden
Hyphodontia pachyspora LWZ 20170908-5 China
Hymenochaetaceae
Chaetoporellaceae
Tubulicrinaceae
Umbellaceae
Rigidoporaceae
Hyphodontiaceae

Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of the order Hymenochaetales based on ITS+nLSU sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

0.012875 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS) = 269.5.

The ITS dataset (Fig. 3) comprised 81 specimens representing 56 species of two new species and related taxa in the genus *Lyomyces*. The dataset had an aligned length of 470 characters, of which 209 characters are constant, 35 are variable and parsimony uninformative, and 226 are parsimony informative. Maximum parsimony analysis yielded 6 equally parsimonious trees (TL = 1574, CI = 0.3018, HI = 0.6982, RI = 0.6876, and RC = 0.2075). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.012875 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS) = 269.5.

The ITS dataset (Fig. 4) comprised 28 specimens representing 17 species of new species and related taxa in the genus *Tubulicrinis*. The dataset had an

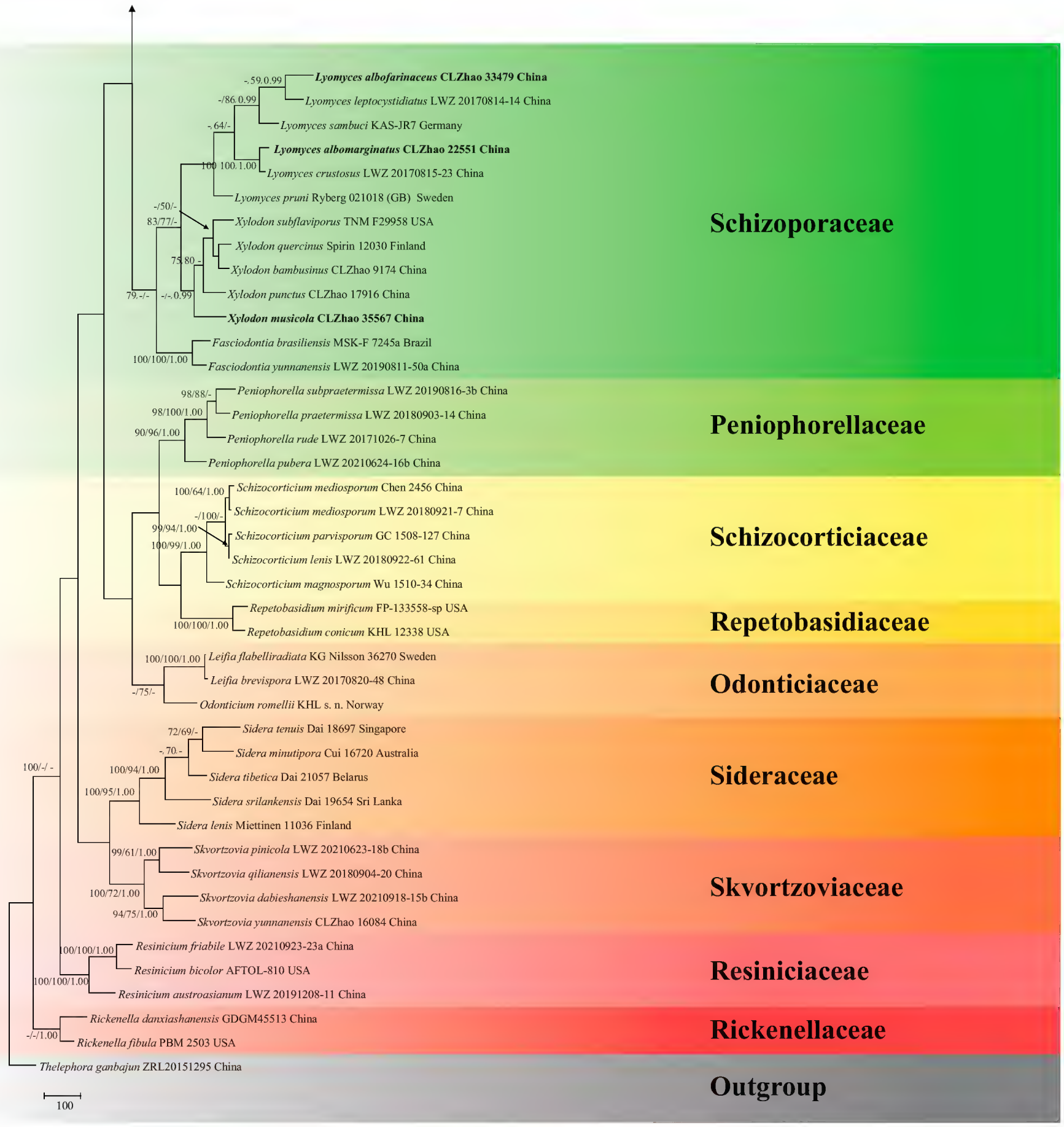
Lyomyces albofarinaceus CLZhao 33479 China
Lyomyces leptocystidiatus LWZ 20170814-14 China
Lyomyces sambuci KAS-JR7 Germany
Lyomyces albomarginatus CLZhao 22551 China
Lyomyces crustosus LWZ 20170815-23 China
Lyomyces pruni Ryberg 021018 (GB) Sweden
Xylodon subflaviporus TNM F29958 USA
Xylodon quercinus Spirin 12030 Finland
Xylodon bambusinus CLZhao 9174 China
Xylodon punctus CLZhao 17916 China
Xylodon musicola CLZhao 35567 China
Fasciodontia brasiliensis MSK-F 7245a Brazil
Fasciodontia yunnanensis LWZ 20190811-50a China
Peniophorella subpraetermissa LWZ 20190816-3b China
Peniophorella praetermissa LWZ 20180903-14 China
Peniophorella rude LWZ 20171026-7 China
Peniophorella pubera LWZ 20210624-16b China
Schizocorticium mediosporum Chen 2456 China
Schizocorticium mediosporum LWZ 20180921-7 China
Schizocorticium parvisporum GC 1508-127 China
Schizocorticium lenis LWZ 20180922-61 China
Schizocorticium magnosporum Wu 1510-34 China
Repetobasidium mirificum FP-133558-sp USA
Repetobasidium conicum KHL 12338 USA
Leifia flabelliradiata KG Nilsson 36270 Sweden
Leifia brevispora LWZ 20170820-48 China
Odonticium romellii KHL s. n. Norway
Sidera tenuis Dai 18697 Singapore
Sidera minutipora Cui 16720 Australia
Sidera tibetica Dai 21057 Belarus
Sidera srilankensis Dai 19654 Sri Lanka
Sidera lenis Miettinen 11036 Finland
Skvortzovia pinicola LWZ 20210623-18b China
Skvortzovia qilianensis LWZ 20180904-20 China
Skvortzovia dabieshanensis LWZ 20210918-15b China
Skvortzovia yunnanensis CLZhao 16084 China
Resinicium friabile LWZ 20210923-23a China
Resinicium bicolor AFTOL-810 USA
Resinicium austroasianum LWZ 20191208-11 China
Rickenella danxiashanensis GDGM45513 China
Rickenella fibula PBM 2503 USA
Thelephora ganbajun ZRL20151295 China
100
Schizoporaceae
Peniophorellaceae
Schizocorticiaceae
Repetobasidiaceae
Odonticiaceae
Sideraceae
Skvortzoviaceae
Resiniciaceae
Rickenellaceae
Outgroup

Figure 1. Continued.

aligned length of 772 characters, of which 284 characters are constant, 152 are variable and parsimony uninformative, and 336 are parsimony informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 1409, CI = 0.5777, HI = 0.4223, RI = 0.6248, and RC = 0.3610). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.006683 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double the average ESS (avg ESS) = 633.

The ITS dataset (Fig. 5) comprised 104 specimens representing 97 species of the new species and related taxa in the genus *Xylodon*. The dataset had an aligned length of 673 characters, of which 233 characters are constant, 81 are variable and parsimony uninformative, and 359 are parsimony informative. Maximum parsimony analysis yielded 5,000 equally parsimonious trees

Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of the one new species and related species in the genus *Hymenochaete* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

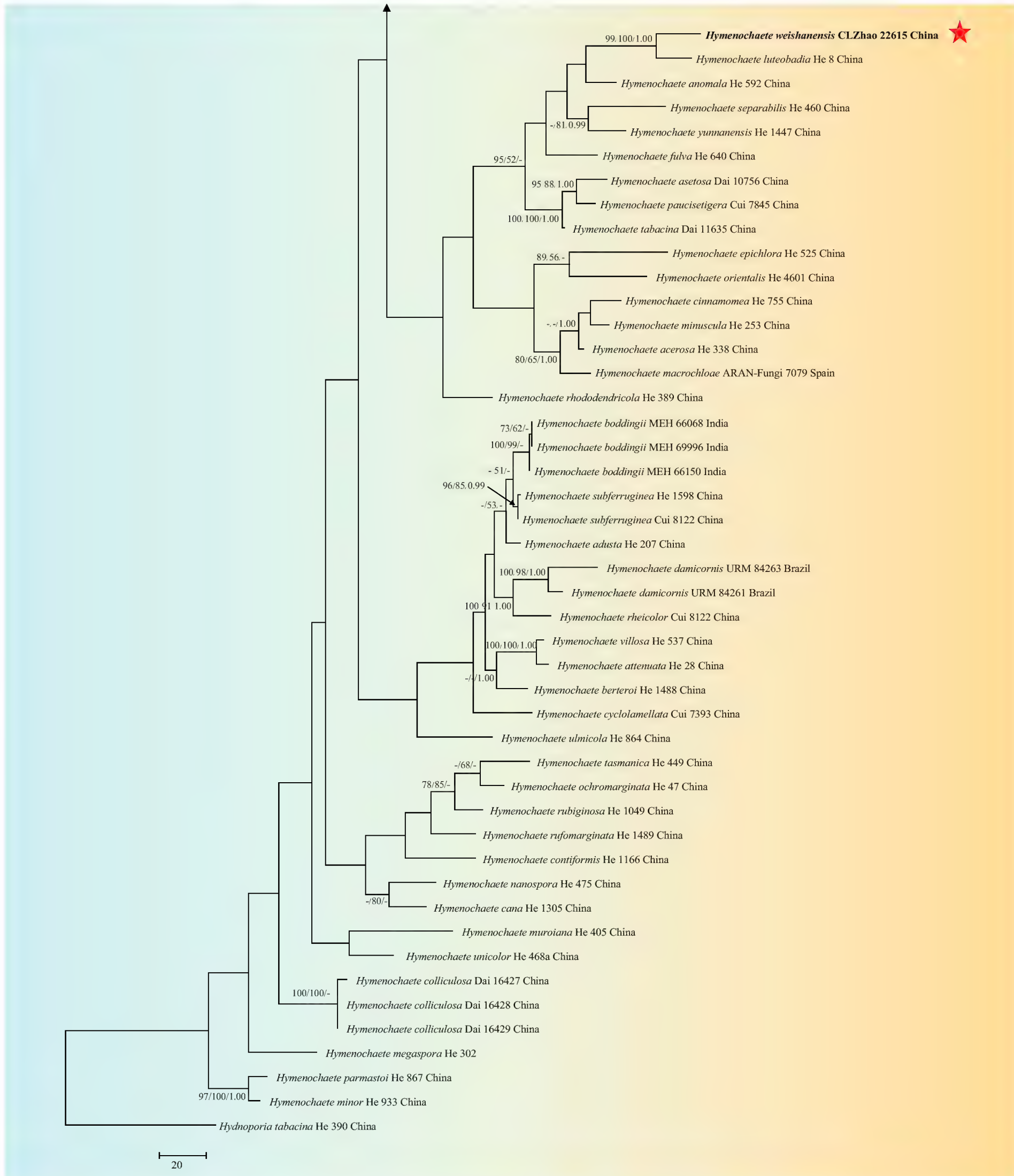

Figure 2. Continued.

(TL = 3842, CI = 0.2140, HI = 0.7860, RI = 0.4337, and RC = 0.0928). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.022556 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is double of the average ESS (avg ESS) = 1143.5.

Figure 3. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Lyomyces* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

Figure 3. Continued.

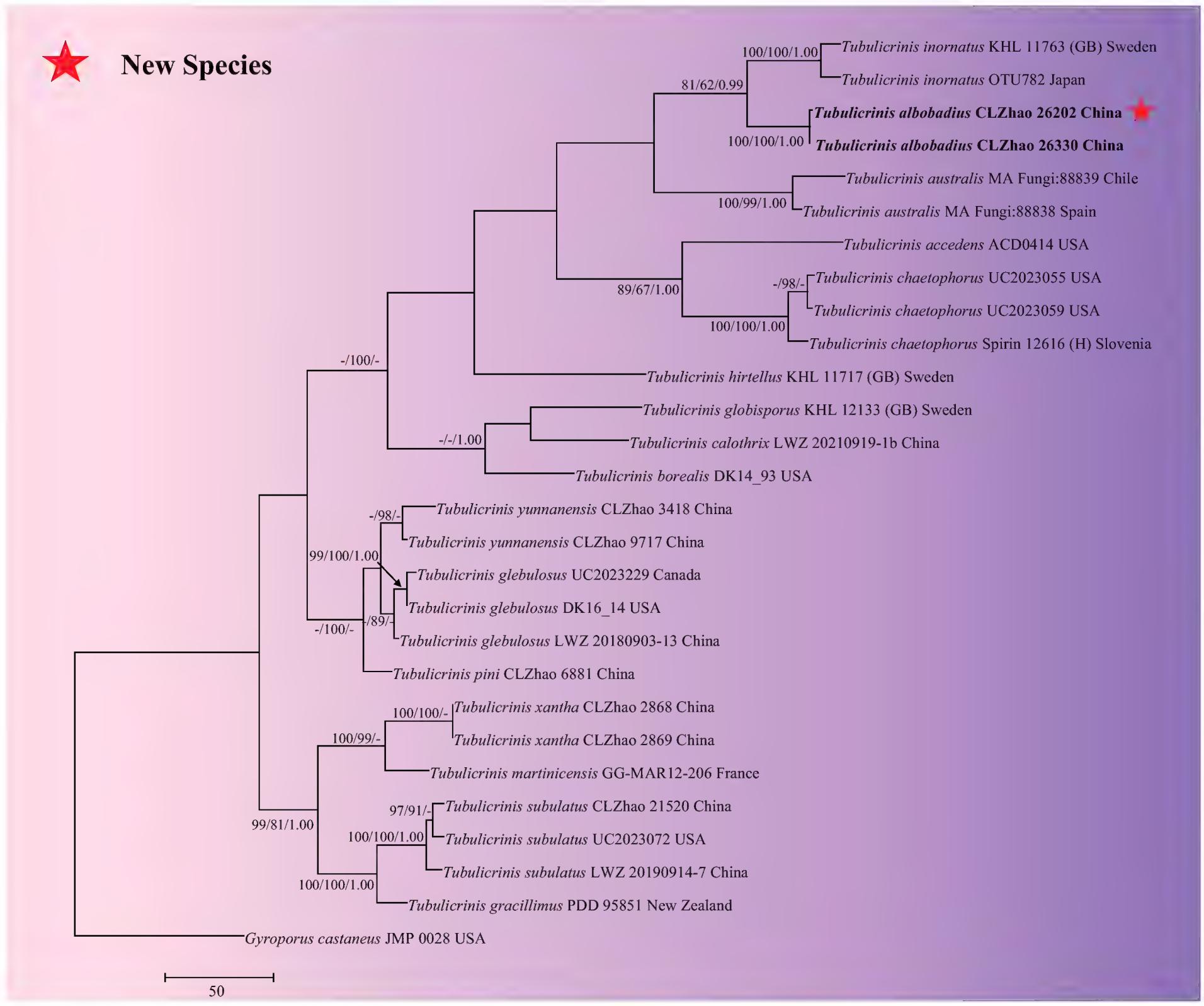

Figure 4. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Tubulicrinis* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

The phylogram based on the combined ITS+nLSU sequences (Fig. 1) analysis showed that five new species *Hymenochaete weishanensis*, *Lyomyces albofarinaceus*, *Lyomyces albomarginatus*, *Tubulicrinis albobadius* and *Xylodon musicola* were assigned to the genera *Hymenochaete*, *Lyomyces*, *Tubulicrinis* and *Xylodon* within the order Hymenochaetales, individually. The phylogenetic tree based on ITS sequences (Fig. 2), revealed that *H. weishanensis* was retrieved as a sister to *H. luteobadia*. The taxon based on the ITS sequences (Fig. 3) revealed that *L. albofarinaceus* was grouped with *L. albopulverulentus* and *L. qujingensis*. *L. albomarginatus* was sister to *L. crustosus*. The topology based on the ITS sequences (Fig. 4), revealed that *T. albobadius* was grouped with *T. australis* and *T. inornatus*. The phylogenetic tree, based on ITS sequences (Fig. 5), revealed that *X. musicola* grouped with three taxa: *X. gloeocystidiifer*, *X. hydnoides*, and *X. neotropicus*.

Figure 5. Maximum parsimony strict consensus tree illustrating the phylogeny of the new species and related species in the genus *Xylodon* based on ITS sequences. Branches are labelled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

Figure 5. Continued.

Taxonomy

***Hymenochaete weishanensis* Y.F. Dai & C.L. Zhao, sp. nov.**

MycoBank No: 856316

Figs 6, 7

Holotype. China • Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao Village, GPS coordinates 25°02'N, 100°16'E, evel. 1910 m a.s.l., on a fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2022, CLZhao 22615 (SWFC).

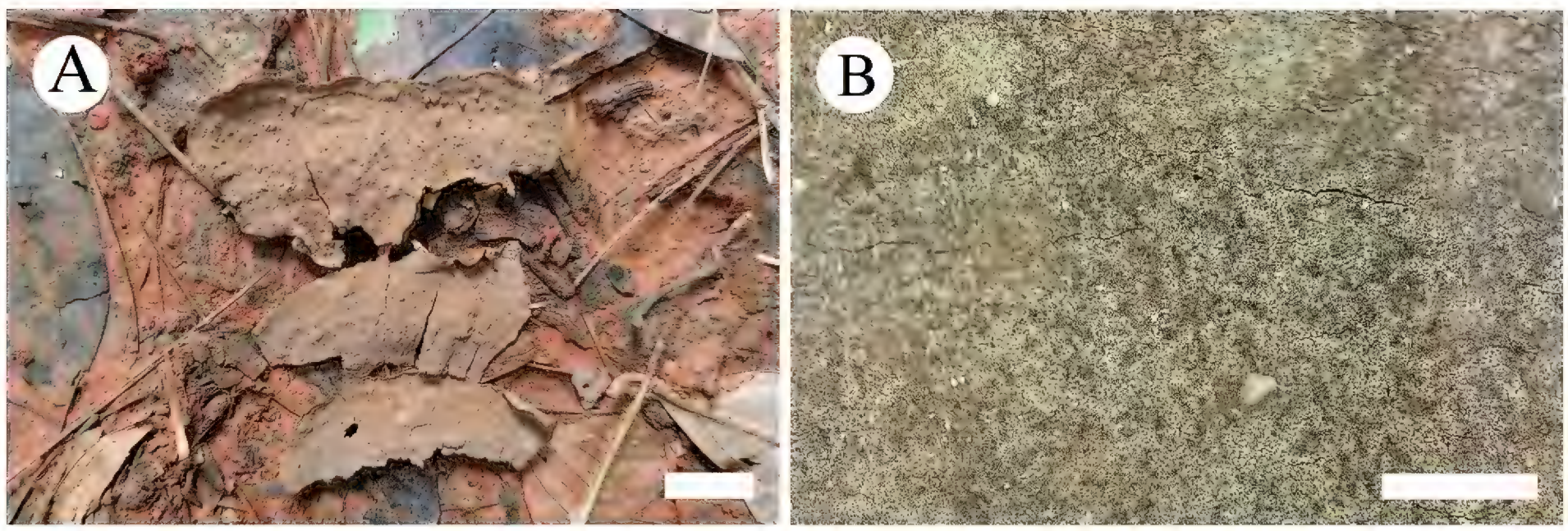

Figure 6. Basidiomata of *Hymenochaete weishanensis* in general and detailed views (CLZhao 22615, holotype). Scale bars: 1cm (**A**); 1mm (**B**).

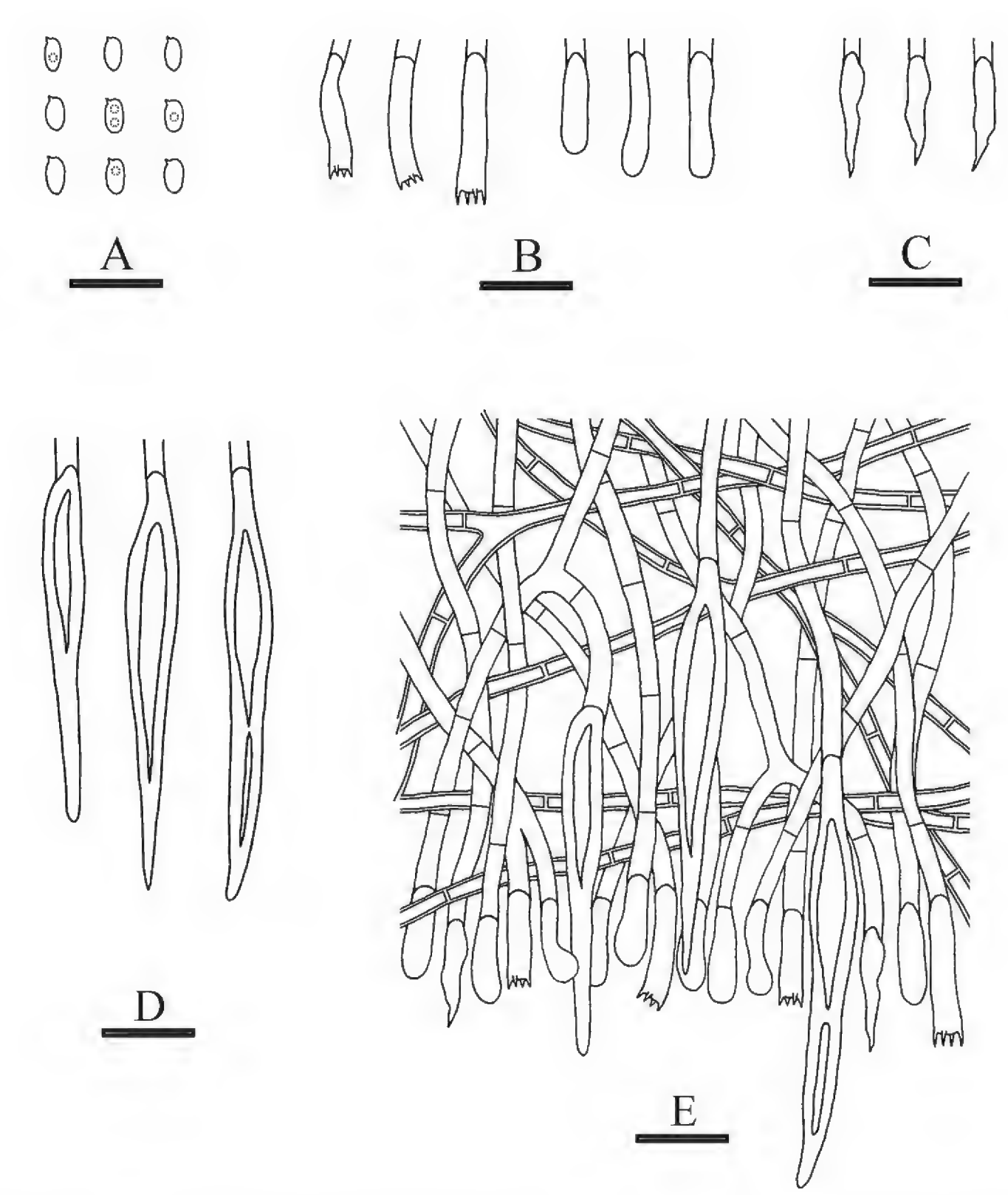

Figure 7. Microscopic structures of *Hymenochaete weishanensis* (holotype, CLZhao 22615). **A** Basidiospores **B** basidia and basidioles **C** tapering cystidia **D** setae **E** part of the vertical section of hymenium. Scale bars: 10 μm (**A–E**).

Etymology. *weishanensis* (Lat.), refers to the locality (Weishan) of the holotype.

Basidiomata. Annual, effused-reflexed, thin, coriaceous, without odor or taste when fresh, up to 5 cm long, 2.5 cm wide, and 150 μm thick. Pileal surface dark brown upon drying. Hymenial surface tuberculate, lightly brown when fresh, turning to gray brown upon drying. Sterile margin narrow, slightly gray-brown, up to 1 mm wide.

Hyphal system. Monomitic, generative hyphae with simple-septa, colorless, thin to slightly thick-walled, frequently branched, interwoven, 2.0–2.8 μm in diameter, IKI–, CB–; tissues unchanged in KOH.

Hymenium. Cystidia tapering, thin-walled, smooth, 9.5–20.5 × 2.0–3.5 μm; cystidioles absent. Hymenial setae abundant, subulate, reddish brown, thick-walled, smooth, 33.0–61.5 × 5.0–8.5 μm, projecting above the hymenium. Basidia subclavate, colorless, thin-walled, simple-septum, with four sterigmata, 6.5–24.0 × 2.5–4.0 μm; basidioles in shape similar to basidia, but slightly smaller.

Basidiospores. Elipsoid to narrow ellipsoid, colorless, thin-walled, smooth, with one or two guttate, IKI–, CB–, 4.0–5.0(–5.5) × 2.0–3.0 μm, L = 4.76 μm, W = 2.52 μm, Q = 1.86–1.92 (n = 60/2).

Additional specimens examined (Paratype). CHINA • Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao Village, on a fallen angiosperm branch, 19 July 2022, CLZhao 40297 (SWFC).

***Lyomyces albofarinaceus* Y.F. Dai & C.L. Zhao, sp. nov.**

MycoBank No: 856317

Figs 8, 9

Holotype. CHINA • Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, GPS coordinates 28°05'N, 104°20'E, evel. 1600 m a.s.l., on a fallen branch of angiosperm, leg. C.L. Zhao, 20 September 2023, CLZhao 33479 (SWFC).

Etymology. *albofarinaceus* (Lat.), refers to the white and pruinose hymenophore surface.

Basidiomata. Annual, resupinate, adnate, without odor or taste when fresh, up to 8 cm long, 3.5 cm wide, and 150 μm thick. Hymenial surface pruinose, smooth, white when fresh, to white to cream upon drying. Sterile margin narrow, white, up to 1 mm wide.

Hyphal system. Monomitic, generative hyphae with clamp connections, colorless, thin to slightly thick-walled, frequently branched, interwoven, 2.0–3.0 μm in diameter, IKI–, CB–; tissues unchanged in KOH, subhymenial hyphae densely covered by crystals.

Hymenium. Cystidia of two types: (1) tapering, thin-walled, smooth to be covered by crystals, 11.5–44.0 × 4.5–7.5 μm; (2) capitate, thin-walled, smooth to be covered by crystals, slightly constricted at the neck, with a globose tip, 23.5–40.0 × 3.5–5.5 μm; cystidioles absent. Basidia clavate, colorless, thin-walled, with four sterigmata, 15.0–27.0 × 5.0–9.5 μm; basidioles in shape similar to basidia, but slightly smaller.

Basidiospores. Broadly ellipsoid, colorless, thin-walled, smooth, with one guttate, IKI–, CB–, (5.5–)6.0–7.0(–7.5) × (4.5–)5.0–6.0(–6.5) μm, L = 6.46 μm, W = 5.62 μm, Q = 1.07–1.15 (n = 60/2).

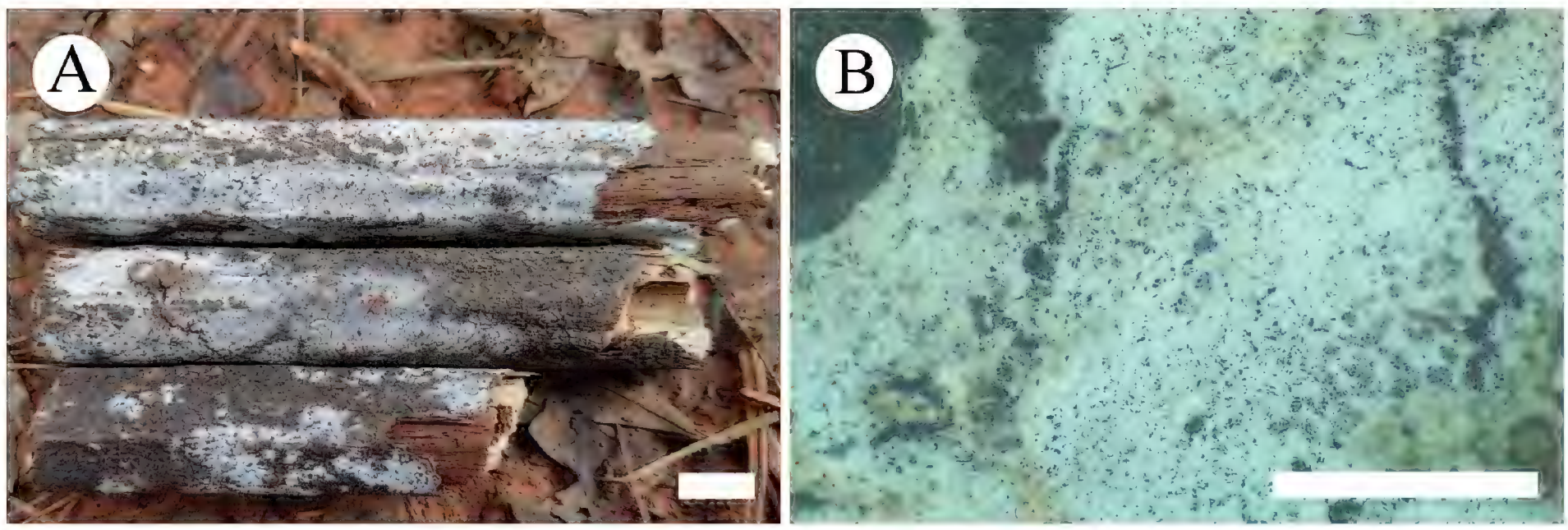

Figure 8. Basidiomata of *Lyomyces albofarinaceus* in general and detailed views (CLZhao 33479, holotype). Scale bars: 1cm (**A**); 1mm (**B**).

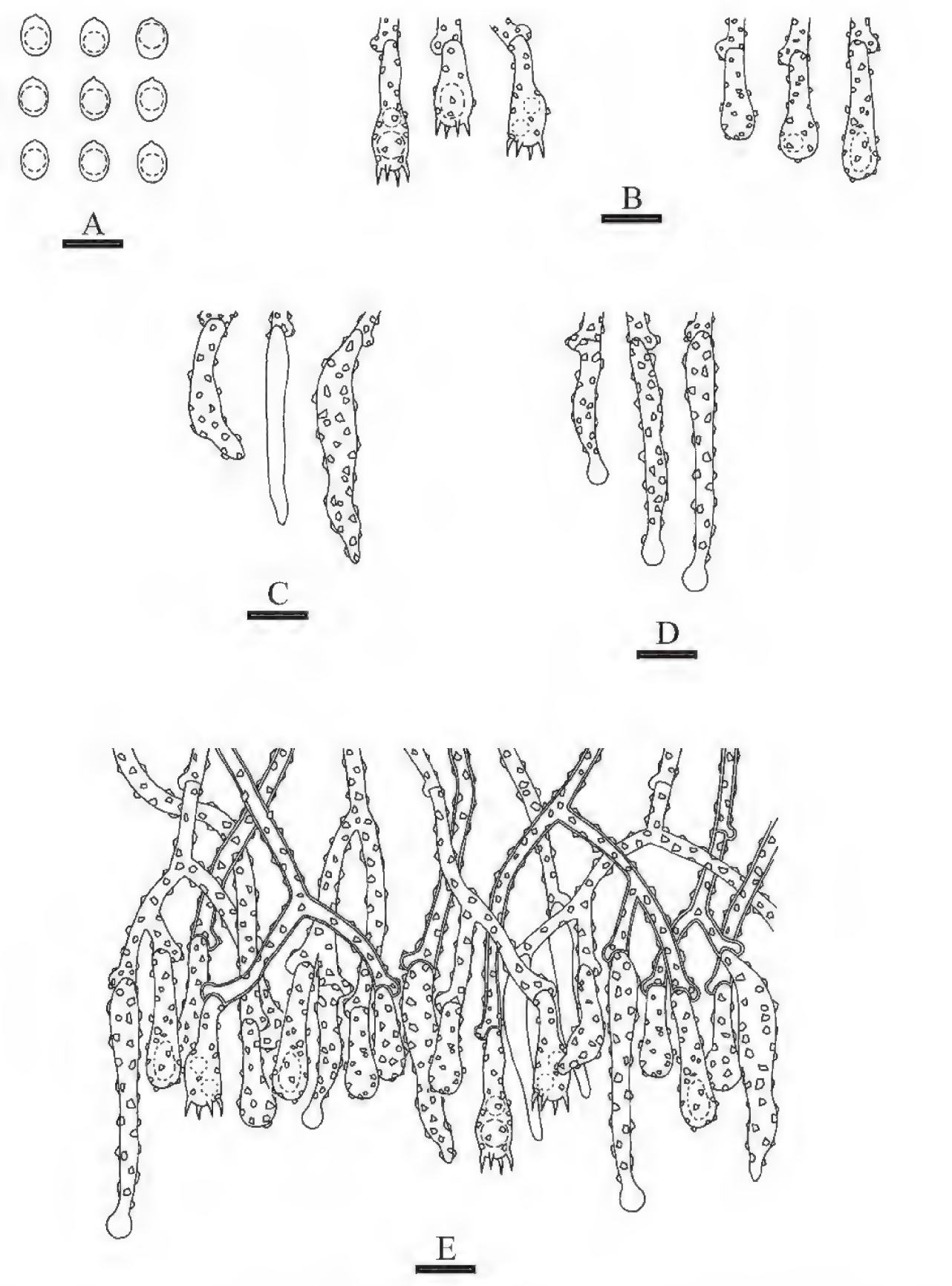

Figure 9. Microscopic structures of *Lyomyces albofarinaceus* (holotype, CLZhao 33479). **A** Basidiospores **B** basidia and basidioles **C** tapering cystidia **D** Capitate cystidia **E** part of the vertical section of hymenium. Scale bars: 10 μm (**A–E**).

Additional specimens examined (Paratype). CHINA • Yunnan Province, Qujing, Qilin District, Cuishan Forestry Park, on a fallen angiosperm branch, 5 November 2022, CLZhao 26661 (SWFC).

***Lyomyces albomarginatus* Y.F. Dai & C.L. Zhao, sp. nov.**

MycoBank No: 856737

Figs 10, 11

Holotype. CHINA • Yunnan Province, Dali, Weishan County, QinghuaTown, Green Peacock Reserve, Jiangzui Village, GPS coordinates 25°01'N, 100°11'E, evel. 1500 m a.s.l., on a fallen branch of angiosperm, leg. C.L. Zhao, 18 July 2022, CLZhao 22551 (SWFC).

Etymology. *albomarginatus* (Lat.), refers to the white margin of the basidiomata.

Basidiomata. Annual, resupinate, adnate, without odor or taste when fresh, up to 8 cm long, 3 cm wide, and 150 μm thick. Hymenial surface cracked, slightly buff when fresh, turning to buff to slightly yellowish upon drying. Sterile margin slightly buff, up to 3 mm wide.

Hyphal system. Monomitic, generative hyphae with clamp connections, colorless, thin to slightly thick-walled, rarely branched, interwoven, 2.0–3.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH.

Hymenium. Cystidia numerous, tapering, thin-walled, smooth, 22.5–30.0 × 2.0–4.0 μm; cystidioles absent. Basidia cylindrical, colorless, thin-walled, with four sterigmata, 15.0–19.0 × 3.5–4.3 μm; basidioles in shape similar to basidia, but slightly smaller.

Basidiospores. Elliposoid, colorless, thin-walled, smooth, with one guttate, IKI–, CB–, (3.5–)4.0–5.5(–6.0) × (2.5–)2.7–3.5(–3.7) μm, L = 4.89 μm, W = 3.13 μm, Q = 1.56 (n = 30/1).

***Tubulicrinis albobadius* Y.F. Dai & C.L. Zhao, sp. nov.**

MycoBank No: 856318

Figs 12, 13

Holotype. CHINA • Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, GPS coordinates 25°32'N, 103°42'E, evel. 2250 m a.s.l., on a fallen branch of angiosperm, leg. C.L. Zhao, 5 Novermber 2022, CLZhao 26202 (SWFC).

Etymology. *albobadius* (Lat.), refers to the white basidiomata.

Basidiomata. Annual, resupinate, thin, adnate, without odor or taste when fresh, up to 8 cm long, 1.5 cm wide, and 150 μm thick. Hymenial surface arachnoid, white when fresh and became white to gray when drying. Sterile margin narrow, white, up to 1 mm.

Hyphal system. Monomitic, generative hyphae with clamp connections, colorless, thick-walled, branched, interwoven, 2.0–4.0 μm in diameter, IKI–, CB–; tissues unchanged in KOH.

Hymenium. Cystidia and cystidioles absent. Lyocystidia projecting, thick-walled, with a globose tip, some of the globose tips are thin-walled, 38.0–71.0 × 8.3–10.0 μm. Basidia barred, colorless, thin-walled, with four sterigmata, 9.5–14.0 × 4.0–5.0 μm; basidioles in shape similar to basidia, but slightly smaller.

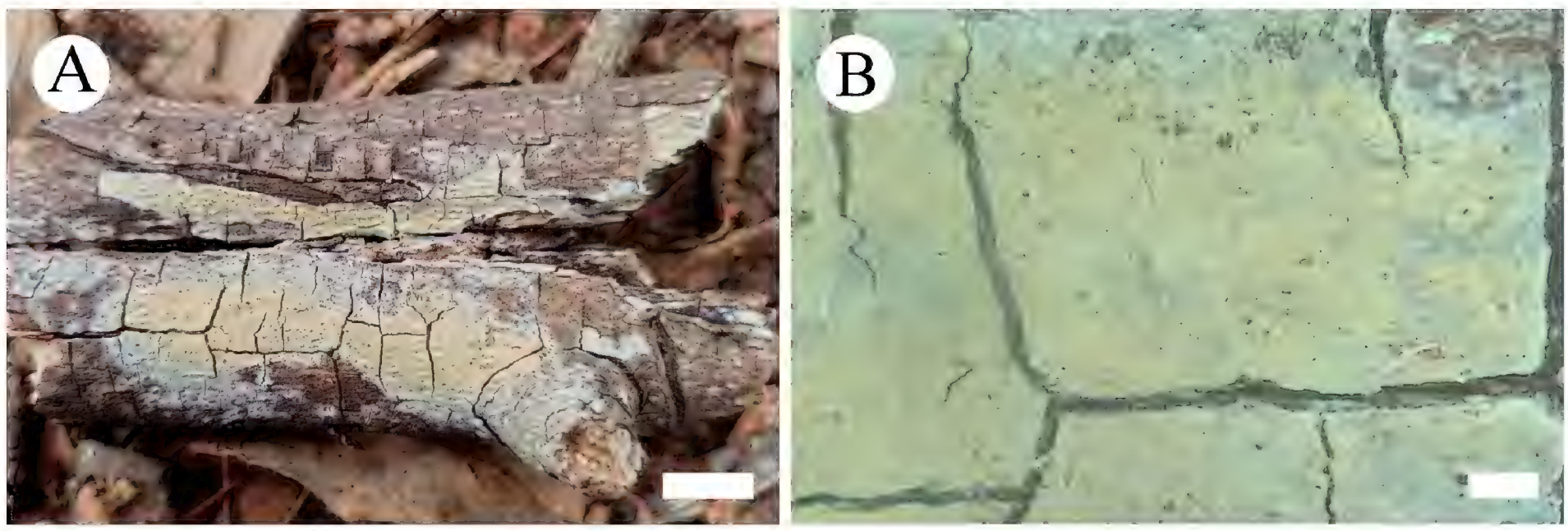

Figure 10. Basidiomata of *Lyomyces albomarginatus* in general and detailed views (CLZhao 22551, holotype). Scale bars: 1cm (**A**); 1mm (**B**).

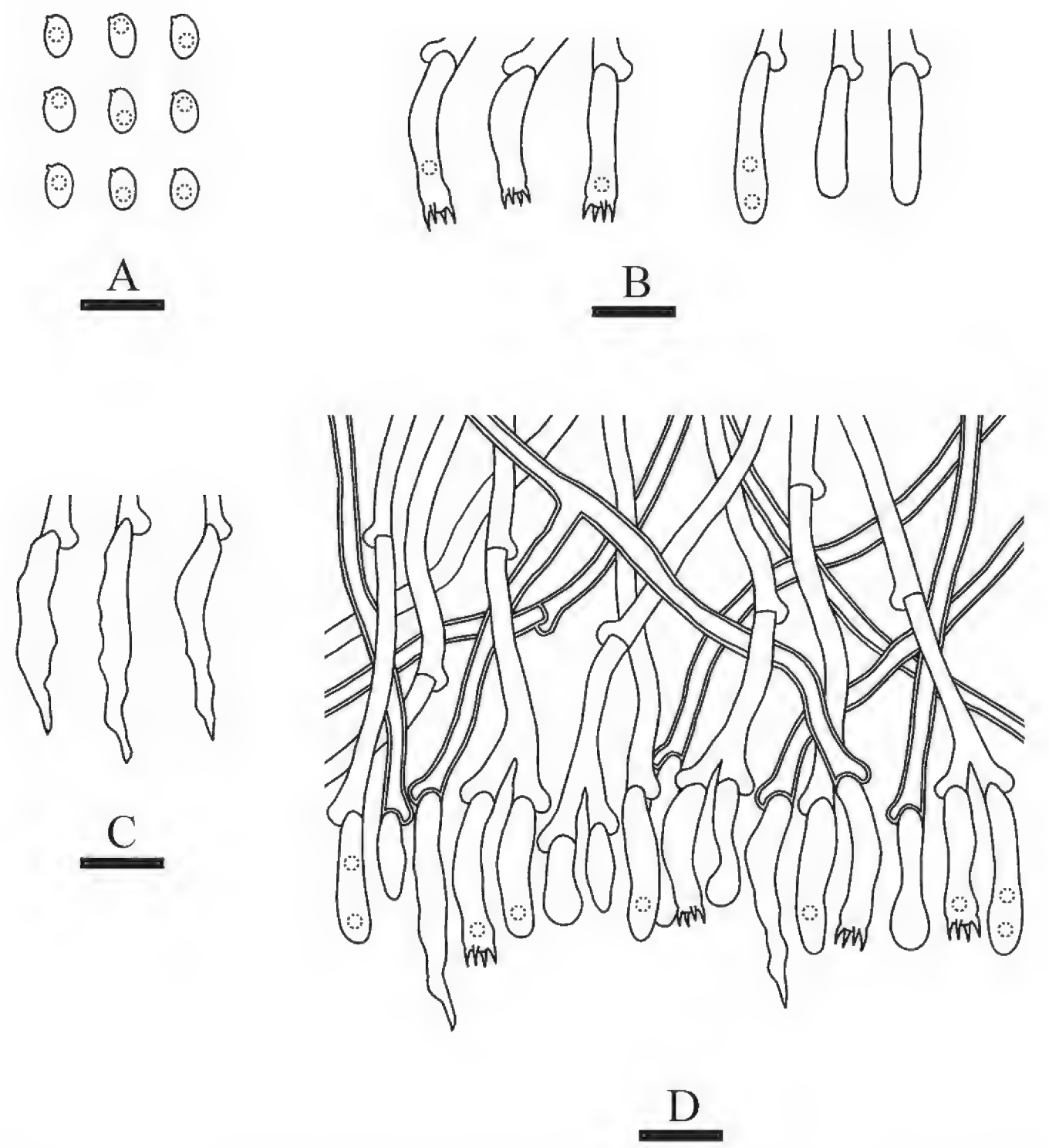

Figure 11. Microscopic structures of *Lyomyces albomarginatus* (holotype, CLZhao 22551). **A** Basidiospores **B** basidia and basidioles **C** tapering cystidia **D** part of the vertical section of hymenium. Scale bars: 10 μm (**A–D**).

Basidiospores. Cylindrical to allantoid, colorless, thin-walled, smooth, with one or two guttate, IKI–, CB–, (3.5–)4.0–6.0(–6.5) × 1.5–2.2(–2.5) μm, L = 5.09 μm, W = 1.89 μm, Q = 2.55–2.77 (n = 60/2).

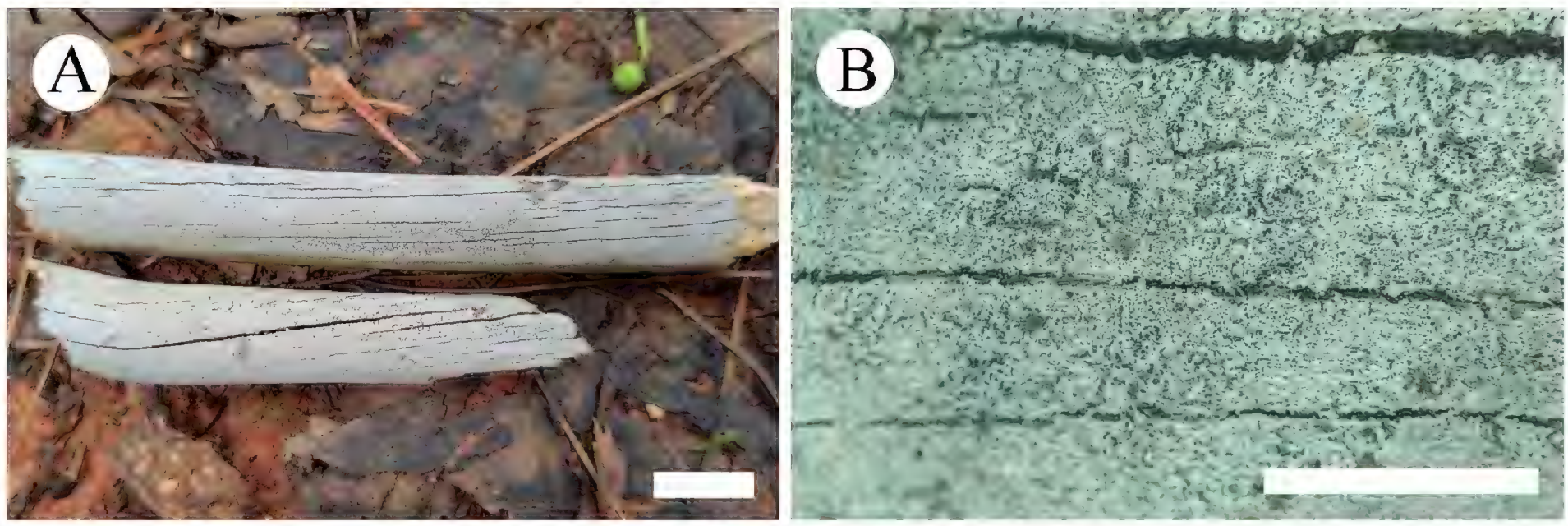

Figure 12. Basidiomata of *Tubulicrinis albobadius* in general and detailed views (CLZhao 26202, holotype). Scale bars: 1cm (**A**); 1mm (**B**).

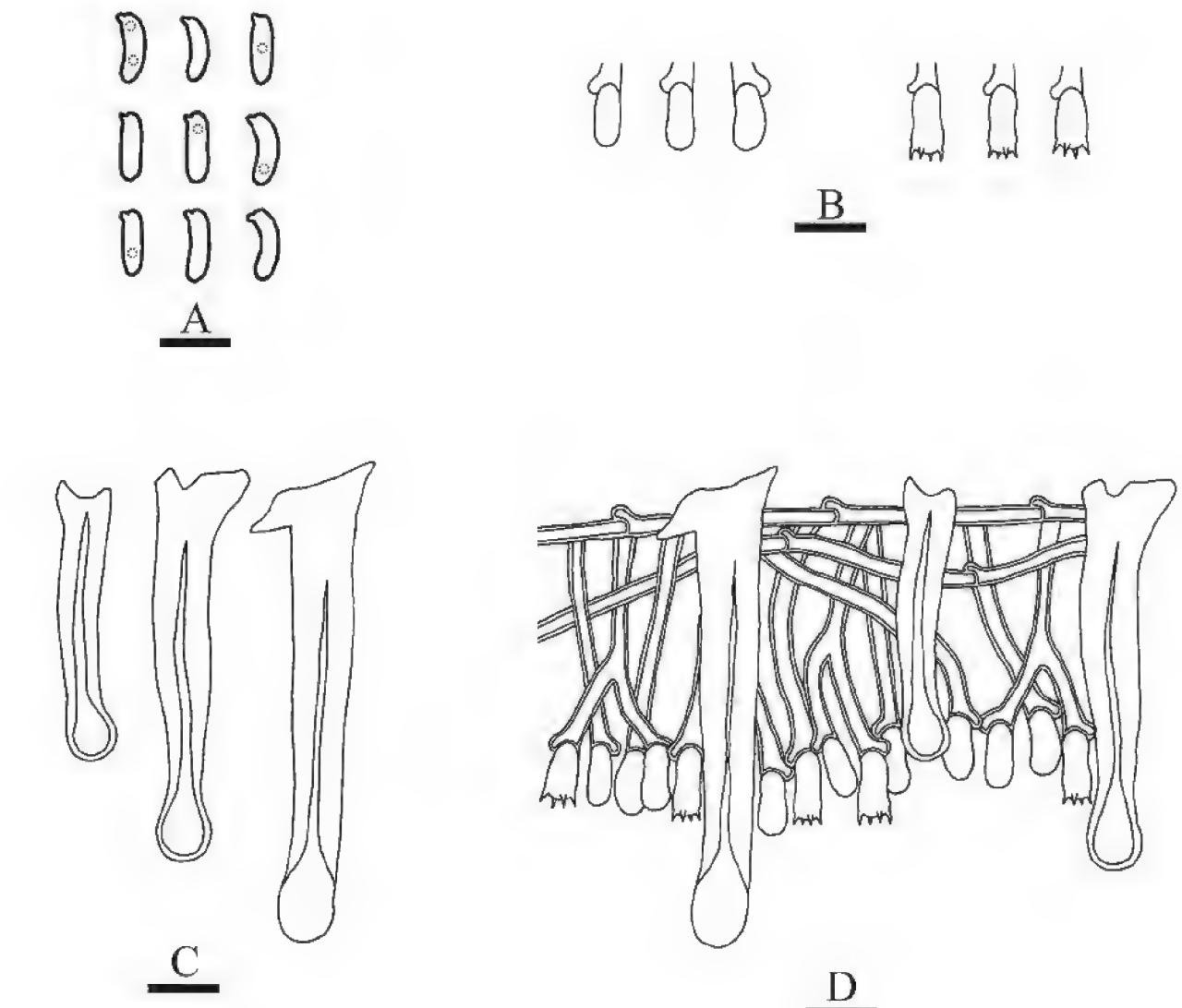

Figure 13. Microscopic structures of *Tubulicrinis albobadius* (holotype, CLZhao 26202). **A** Basidiospores **B** basidia and basidioles **C** lyocystidia **D** part of the vertical section of hymenium. Scale bars: 5 μm (**A**); 10 μm (**B–D**).

Additional specimens examined (Paratype). China • Qujing, Qilin District, Cuishan Forest Park, on a fallen angiosperm branch, 5 November 2022, CLZhao 26330 (SWFC).

***Xylodon musicola* Y.F. Dai & C.L. Zhao, sp. nov.**

MycoBank No: 856319

Figs 14, 15

Holotype. China • Yunnan Province, Zhaotong, Yongshan County, Mugan Town, Wumengshan Nature Reserve, GPS coordinates 28°05'N, 103°58'E, evel.

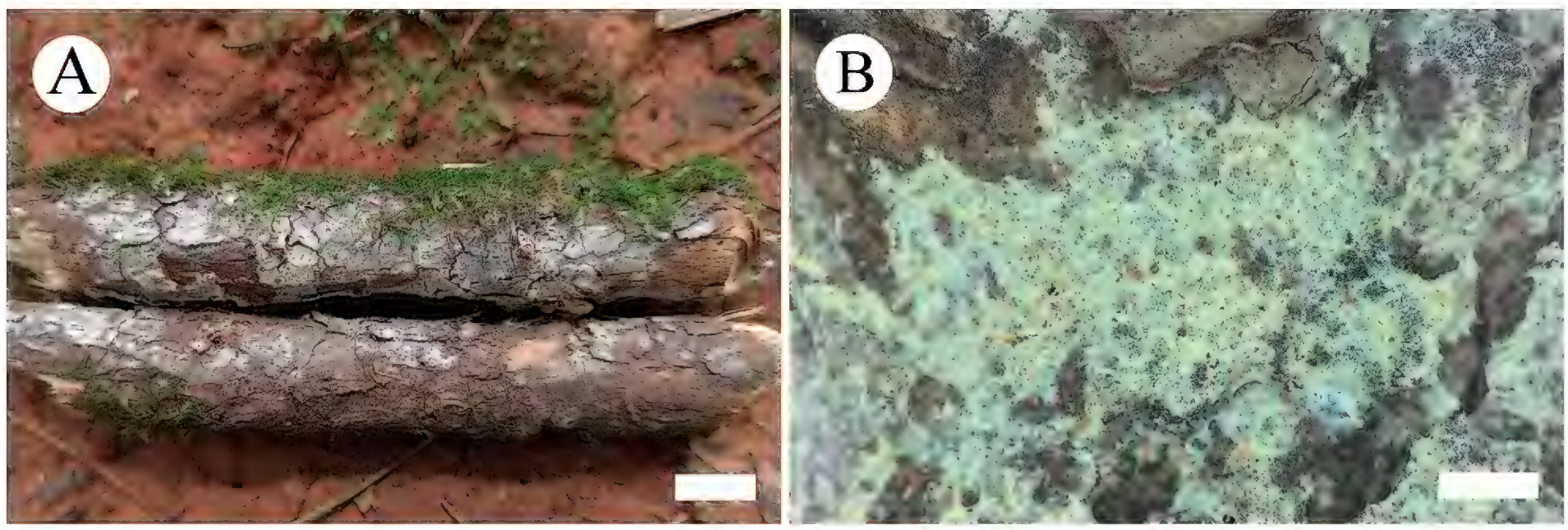

Figure 14. Basidiomata of *Xylodon musicola* in general and detailed views (CLZhao 35567, holotype). Scale bars: 1cm (**A**); 1mm (**B**).

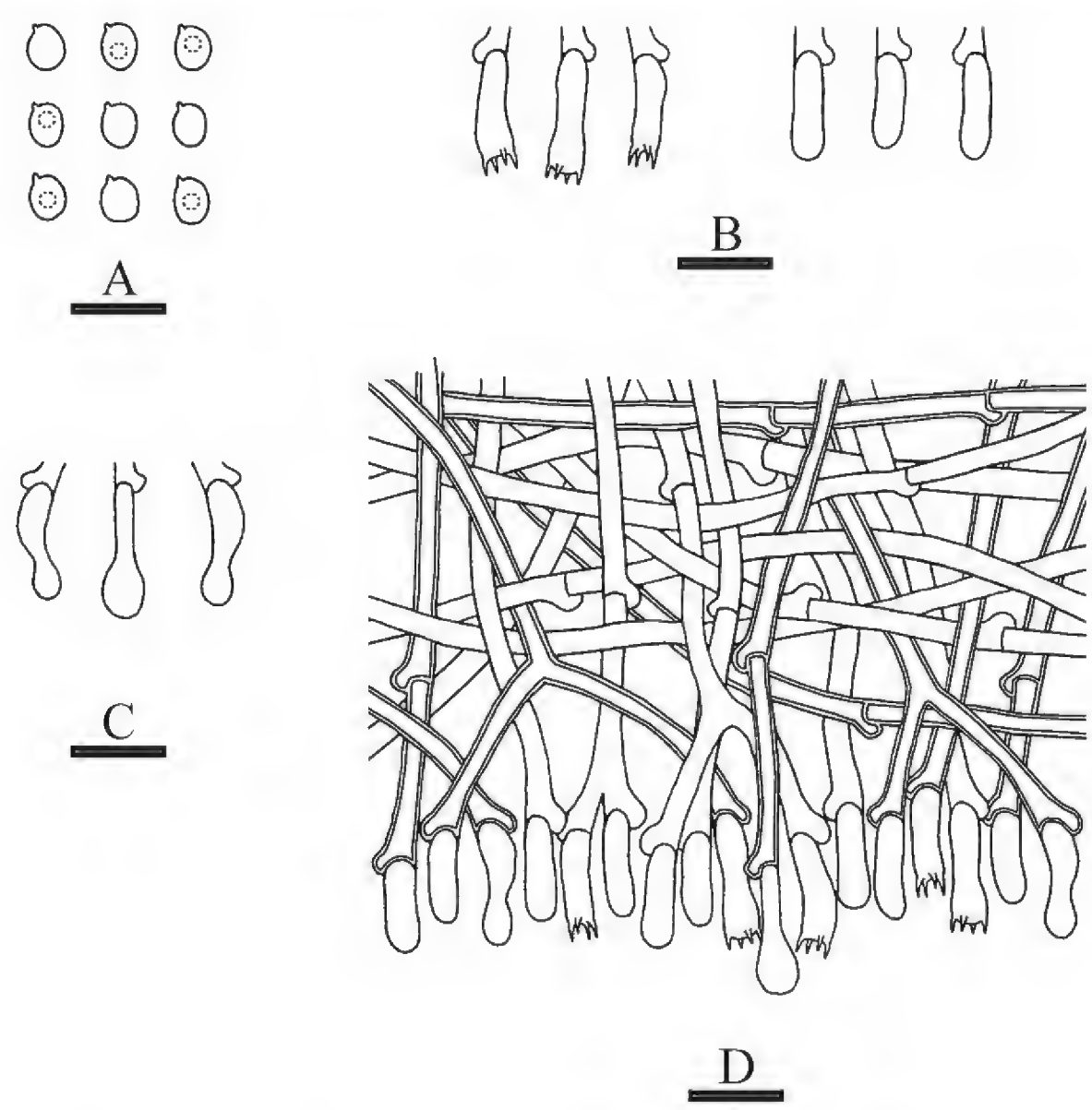

Figure 15. Microscopic structures of *Xylodon musicola* (holotype, CLZhao 35567). **A** Basidiospores **B** basidia and basidioles **C** capitate cystidia **D** part of the vertical section of hymenium. Scale bars: 10 μm (**A–D**).

2200 m a.s.l., on a fallen angiosperm branch, leg. C.L. Zhao, 7 November 2023, CLZhao 35567 (SWFC).

Etymology. *musicola* (Lat.), refers to the growth on the mosses, which is located Bryophyta.

Basidiomata. Annual, resupinate, adnate, very difficult to separate from substrate, without odor or taste when fresh, up to 7 cm long, 2 cm wide, and 150 μm thick. Hymenial surface arachnoid, white when fresh and becoming white to cream when drying. Sterile margin narrow, slightly cream, up to 1 mm wide. The basidiomata grow on the surface of muscus.

Hyphal system. Monomitic, generative hyphae with clamp connections, colorless, thin to slightly thick-walled, rarely branched, interwoven, 2.5–4.0 µm in diam, IKI–, CB–; tissues unchanged in KOH.

Hymenium. Cystidia capitate, thin-walled, smooth, slightly constricted at the neck, with a globose tip, 12.5–20.0 × 3.5–5.0 µm; cystidioles absent. Basidia clavate, colorless, thin-walled, with four sterigmata, 11.0–15.5 × 3.5–5.0 µm; basidioles in shape similar to basidia, but slightly smaller.

Basidiospores. Broadly ellipsoid to globe, colorless, thin-walled, smooth, with one guttate, IKI–, CB–, 4.0–5.5(–6.0) × 3.5–5.0(–5.5) µm, L = 4.77 µm, W = 4.35 µm, Q = 1.07–1.13 (n = 60/2).

Additional specimens examined (Paratype). CHINA • Yunnan Province, Zhaotong, Yongshan County, Mugan Town, Wumengshan Nature Reserve, on a fallen angiosperm branch, 7 November 2023, CLZhao 40298 (SWFC).

Discussion

The order Hymenochaetales comprises many representative corticioid fungal taxa, including hydnoid, corticioid, and polyporoid fungi possessing basidiomata with diverse hymenophoral and cystidial morphology (Riebesehl et al. 2019; Wu et al. 2022; Guan et al. 2023; Zhang et al. 2024). In the present study, five new species *Hymenochaete weishanensis*, *Lyomyces albofarinaceus*, *L. albomarginatus*, *Tubulicrinis albobadius*, and *Xylodon musicola* are described based on the phylogenetic analyses and morphological characteristics.

Based on ITS topology (Fig. 2), *Hymenochaete weishanensis* grouped closely with two species *H. luteobadia* and *H. anomala*. However, *H. anomala* can be delimited from *H. weishanensis* by its smooth hymenial surface and narrower basidiospores (3.5–4.5 × 1.8–2.3 µm; Parmasto 2001). *Hymenochaete Luteobadia* differs from *H. weishanensis* due to its sulcate and zonate hymenial surface and wider basidia (15.0–20.0 × 4.0–5.0 µm; Parmasto 2001). Based on ITS topology (Fig. 3), the taxon *Lyomyces albofarinaceus* grouped closely with *L. albopulverulentus* and *L. qujingensis*. The taxon *L. albomarginatus* was sister to *L. crustosus*. However, *L. qujingensis* differs from *L. albofarinaceus* due to its longer capitate cystidia (40.0–60.0 × 4.0–7.5 µm) and by possessing clavate cystidia (16.5–18.0 × 7.5–8.5 µm; Dong et al. 2024). *L. albopulverulentus* can be delimited from *L. albofarinaceus* by its longer basidiospores (8.0–10.5 × 5.5–7.0 µm; Guan et al. 2023). *Lyomyces crustosus* can be delimited from *L. albomarginatus* due to its odontoid hymenial surface and longer basidia (20–30 × 4.0–5.0 µm; Maekawa 1994). Based on ITS topology (Fig. 4), the taxon *Tubulicrinis albobadius* grouped closely with *T. australis* and *T. inornatus*. However, *T. inornatus* differs from *T. albobadius* by its reticulate to porulose hymenial surface and wider basidiospores (4.0–5.0 × 2.5–3.5 µm; Maekawa 2021). Based on ITS topology (Fig. 5), the taxon *Xylodon musicola* grouped closely with *X. gloeocystidiifer*, *X. hydnoides* and *X. neotropicus*. However, morphologically, *X. gloeocystidiifer* differs from *X. musicola* by its odontioid hymenial surface and smaller basidiospores (3.5–4.0 × 2.8–3.5 µm; Yurchenko et al. 2024b), *X. hydnoides* differs from *X. musicola* by its hydnoid hymenial surface and by possessing clavate cystidia (29.5–38.5 × 3.5–4.5 µm; Dong et al. 2024). *Xylodon neotropicus* can be delimited from *X.*

musicola due to its odontioid to short hydnoid hymenial surface and shorter basidiospores (3.5–4.0 × 3.3–3.7 µm; Yurchenko et al. 2024b).

Morphologically, *Hymenochaete weishanensis* resembles *H. colliculosa* (Sacc.) Parmasto, *H. biformisetosa* Jiao Yang & S.H. He and *H. sharmae* Hembrom, K. Das & A. Parihar by ellipsoid basidiospores. However, *H. colliculosa* differs from *H. weishanensis* due to its dimitic hyphal system and wider basidia (20.0–24.0 × 5.0–6.0 µm; He et al. 2017). The species *H. biformisetosa* differs from *H. weishanensis* by its smooth hymenial surface and wider basidiospores (4.3–6.0 × 3.0–4.2 µm; Yang and He 2014). The taxon *H. sharmae* differs from *H. weishanensis* by its smooth hymenial surface and wider basidia (12.0–16.0 × 4.0–6.0 µm; Wang et al. 2019)

Morphologically, *Lyomyces albofarinaceus* resembles *L. incanus* J.H. Dong & C.L. Zhao, *Lyomyces lancangjiangensis* Q. Li & C.L. Zhao, and *L. yunnanensis* C.L. Zhao by ellipsoid basidiospores. However, *L. lancangjiangensis* differs from *L. albofarinaceus* due to its membranaceous hymenial surface and narrower basidia (13.0–23.0 × 3.0–4.5 µm; Li et al. 2024b). The taxon *L. incanus* differs from *L. albofarinaceus* by its furfuraceous hymenial surface and narrower basidiospores (5.0–6.5 × 4.0–5.0 µm; Dong et al. 2024). The species *L. yunnanensis* differs from *L. albofarinaceus* by its grandinioid hymenial surface and narrower basidiospores (5.0–7.0 × 3.0–4.5 µm; Guan et al. 2023).

Morphologically, *Lyomyces albomarginatus* resembles *L. lincangensis* J.H. Dong & C.L. Zhao, *L. luteoalbus* J.H. Dong & C.L. Zhao and *L. sinensis* J.H. Dong & C.L. Zhao by ellipsoid basidiospores. However, *L. lincangensis* differs from *L. albomarginatus* due to its coriaceous hymenial surface and wider basidiospores (4.5–6.5 × 3.5–5.0 µm; Dong et al. 2024). *L. luteoalbus* differs from *L. albomarginatus* due to its membranaceous hymenial surface and shorter tapering cystidia (12.0–17.0 × 2.0–3.5 µm; Dong et al. 2024). *L. sinensis* differs from *L. albomarginatus* due to its coriaceous hymenial surface and wider basidiospores (4.5–6.0 × 3.5–4.5 µm; Dong et al. 2024).

Morphologically, *Tubulicrinis albobadius* resembles *T. hirtellus* (Bourd. & Galz.) John Erikss, *T. orientalis* Parmasto and *T. xantha* C.L. Zhao by cylindrical basidiospores. However, *T. hirtellus* differs from *T. albobadius* due to its porulose hymenial surface and longer basidiospores (7.0–8.5 × 2.0–2.5 µm; Hjortstam et al. 1988). The species *T. orientalis* differs from *T. albobadius* due to its hispidulous hymenial surface and narrower basidia (11.0–16.0 × 3.5–4.0 µm; Maekawa and Nordén 2022). The species *T. xantha* differs from *T. albobadius* by its furfuraceous hymenial surface and longer and narrower lyocystidia (78.0–192.5 × 5.8–7.5 µm; He et al. 2020).

Morphologically, *Xylodon musicola* resembles *X. cremeoparinaceus* Q. Yuan & C.L. Zhao, *X. luteodontioides* Q. Yuan & C.L. Zhao and *X. wumengshanensis* Q. Yuan & C.L. Zhao by ellipsoid basidiospores. However, *X. cremeoparinaceus* differs from *X. musicola* due to its farinaceous hymenial surface and narrower basidiospores (3.5–4.5 × 2.5–3.5 µm; Yuan and Zhao 2024). The species *X. luteodontioides* differs from *X. musicola* due to narrower basidiospores (3.5–4.5 × 2.5–3.5 µm) and by possessing schizopapillate cystidia (29.5–37.0 × 2.5–3.5 µm; Yuan and Zhao 2024). The species *X. wumengshanensis* differs from *X. musicola* due to its bigger basidia (22.5–33.0 × 5.0–5.5 µm) and by possessing fusoid cystidia (14.5–22.0 × 5.5–6.5 µm; Yuan and Zhao 2024).

This discovery of five new species *viz*. *Hymenochaete weishanensis*, *Lyomyces albofarinaceus*, *L. albomarginatus*, *Tubulicrinis albobadius*, and *Xylodon musicola* enrich our knowledge of fungal diversity in the order Hymenochaetales. We anticipate that more undescribed taxa will be discovered throughout China after extensive collection combined with morphological and molecular analyses.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Conceptualization, CZ; methodology, CZ, HY and YD; software, CZ, YD and QY; validation, CZ and YD; formal analysis, CZ and YD; investigation, RL, DL, CZ and YD; resources CZ, RL and HY; writing – original draft preparation, CZ, YD, QY, XY and RL; writing – review and editing, CZ, HY, and YD; visualization, CZ and YD; supervision, CZ and HY; project administration, CZ; funding acquisition, CZ and HY. All authors have read and agreed to the published version of the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text.

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